DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

This application claims priority to patent application U.S. Serial No.

5   09/436,184, filed on November 8, 1999, the contents of which are hereby incorporated by

reference.

Statement as to Federally Sponsored Research

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10 government has certain rights in the invention.

Background of the Invention

Primary malignant central nervous system (CNS) neoplasms, particularly

glioblastomas, are highly fatal due to their aggressive and widespread infiltration of the

brain and resistance to anti-cancer treatments. Although progress has been made in

15 unraveling the pathological mechanisms underlying CNS cancers as well as other cancer

types, tumor specific therapeutic approaches and methods of diagnosis have been largely

elusive.

Summary of the Invention

The invention features a method for diagnosing or inhibiting the growth of a

20 malignant neoplasm in a mammal by contacting a tissue or bodily fluid from the mammal

with an antibody which binds to an human aspartyl (asparaginyl) beta-hydroxylase

(HAAH) polypeptide under conditions sufficient to form an antigen-antibody complex

and detecting the antigen-antibody complex. Malignant neoplasms detected in this

manner include those derived from endodermal tissue, e.g., colon cancer, breast cancer,

25 pancreatic cancer, liver cancer, and cancer of the bile ducts. Neoplasms of the central

nervous system (CNS) such as primary malignant CNS neoplasms of both neuronal and

glial cell origin and metastatic CNS neoplasms are also detected. Brain cancers include

metastatic brain tumors, as well as primary brain tumors such as glioma, astrocytomas, and hemangiomas. Patient derived tissue samples, e.g., biopsies of solid tumors, as well as bodily fluids such as a CNS-derived bodily fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid, are contacted with an HAAH-specific antibody.

5   The invention includes a method of eliciting an immune response or confering an immune response to a tumor cell, e.g., a brain tumor, in a mammal by administering to a mammal an antibody which binds to HAAH or a polynucleotide encoding such an antibody. Preferably, the antibody binds to a site in an extracellular domain (e.g., a site within residues 1-700) of HAAH. The antibody binds to an ectodomain of HAAH

10   (residues 19-75 of SEQ ID NO:2). More preferably, the antibody binds to a catalytic domain of HAAH, e.g., amino acids 650-700 of SEQ ID NO:2. For example, FB50 binds to a polypeptide with the amino acid sequence NPVEDS (residues 286-291 of SEQ ID NO:2). Monoclonal antibody HBOH1 binds to a polypeptide with the amino acid sequenc QPWWTPK (residues 573-579 of SEQ ID NO:2), and monoclonal antibody

15   HBOH-2 binds to a polypeptide containing the amino acid sequence LPEDENLR (residues 613-620 of SEQ ID NO:2). The foregoing antigenic epitopes of HAAH are located on the cell surface of malignant cells. Other HAAH-specific antibodies suitable for passive immunization include 5C7, 5E9, 19B, 48A, 74A, 78A, 86A, HA238A, HA221, HA 239, HA241, HA329, and HA355.

20   The antibody to be administered is a heterodimeric antibody, a single chain antibody, or a high affinity single chain antibody. By high affinity is meant that the antigen-specific binding affinity of the antibody has a K_d in the nanomolar range. Preferably, the binding affinity is in the range of 100 pM or higher affinity. For example, the antibody, antibody fragment, or single chain antibody has an antigen-specific binding

25   affinity in the range of 10^{-10} to 10^{-15} molar.

The antibody, or fragment thereof, activates complement in a patient treated with the antibody. Preferably, the antibody mediates antibody-dependent cytotoxicity of

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tumor cells in the patient treated with the antibody. The antibody, or fragment thereof, is administered alone or conjugated to a cytotoxic agent. In the latter case, binding of the antibody to a tumor cell results in impairment or death of the cell, thereby reducing tumor load. The antibody is conjugated to a radiochemical, or a chemical tag which sensitizes

5   the cell to which it is bound to radiation or laser-mediated killing.

Also within the invention, are methods of inducing an HAAH-specific immune response to reduce tumor growth by active immunization. The method involves administering to a mammal an HAAH polypeptide, e.g., a polypeptide containing the amino acid sequence of SEQ ID NO:2. Immunogenic HAAH fragments are also

10   administered to generate an immune response to a particular portion of HAAH. For example, to generate an antibody response to HAAH on the surface of cells, a polypeptide containing an extracellular domain of HAAH (but lacking an intracellular domain of HAAH) is administered. To generate antibodies, which inhibit HAAH activity, the individual is immunized with a polypeptide containing a catalytic domain of

15   HAAH (e.g., amino acids 650-700 of SEQ ID NO:2). Optionally, the polypeptide compositions contain a clinically-acceptable adjuvant compound. Such adjuvants are generally known in the art, and include oil-emulsions, Freunds Complete and Incomplete adjuvant, Vitamin E, aluminum salts or gels, such as aluminum hydroxide, -oxide or -phosphate, saponins, polymers based on polyacrylic acid, such as carbopols, non-ionic

20   block polymers, fatty acid amines, such as avridin and DDA, polymers based on dextran, such as dextran sulphate and DEAE dextran, muramyldipeptides, ISCOMs (immune stimulating complexes, e.g., as described in European Patent EP 109942), biodegradable microcapsules, liposomes, bacterial immune stimulators, such as MDP and LPS, and glucans. Other adjuvant compounds are known in the art, e.g., described in Altman and

25   Dixon, 1989, Advances in Veterinary Science and Comparative Medicine 33: 301-343). Alum is preferred for human use.

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An HAAH-specific immune response is also induced by administering to a mammal a polynucleotide composition encoding an HAAH polypeptide, or a degenerate variant of the HAAH-encoding polynucleotide. For example, the polynucleotide contains the nucleotide sequence of SEQ ID NO:3, or a degenerate variant thereof, or a fragment thereof encoding a specific immunogenic domain of HAAH. Preferably, the HAAH polypeptide encoded by the polynucleotide (or directly administered polypeptide) is enzymatically nonfunctional. More preferably, the HAAH polynucleotide encodes an HAAH polypeptide that is secreted, e.g., the construct contains a signal sequence for transport out of the cell and into an extracellular space. The HAAH polypeptide lacks an essential histidine. The HAAH polypeptide is a truncated HAAH, which contains the first 650 amino acids of SEQ ID NO:2.

Optionally, the polynucleotide composition contains a transfection-enhancing agent, such as a precipitating agent or a lipid. Preferably, the encoded HAAH polyeptide contains the amino acid sequence of SEQ ID NO:2 (full-length HAAH) or a fragment thereof, which contains an extracellular domain of HAAH and lacks an intracellular domain of HAAH. Preferably, the polynucleotide contains a catalytic domain of HAAH. The HAAH-encoding sequences are operably-linked to a promoter and other regulatory sequences for expression of the polypeptides in target cells. The polypeptide may be directed intracellularly or marked for extracellular expression, or secretion. The polynucleotide directs expression in a target cell, which expresses appropriate accessory molecules for antigen presentation, e.g., major histocompatibility antigens.

Methods for diagnosis include detecting a tumor cell in bodily fluids as well as detecting a tumor cell in tissue (*in vivo* or *ex vivo*). For example, a biopsied tissue is contacted with an HAAH-specific antibody and antibody binding measured. Whole body diagnostic imaging may be carried out to detect microtumors undetectable using conventional diagnostic methods. Accordingly, a method for diagnosing a neoplasm in a mammal is carried out by contacting a tissue, e.g., a lymph node, of a mammal with a

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detectably-labeled antibody which binds to HAAH. An increase in the level of antibody binding at a tissue site compared to the level of binding to a normal nonneoplastic tissue indicates the presence of a neoplasm at the tissue site. For detection purposes, the antibody (or HAAH-binding fragment thereof) is labeled with a non-radioactive tag, a

5   radioactive compound, or a colorimetric agent. For example, the antibody or antibody fragment is tagged with ^{125}I, ^{99}Tc, Gd^{+++}, or Fe^{++}. Green fluorescent protein is used as a colorimetric tag.

        The invention also includes a soluble fragment of HAAH. The soluble HAAH polypeptide contains an extracellular domain and optionally lacks part or all of the

10 cytoplasmic domain or transmembrane domain of HAAH. In one example, the fragment lacks residues 660-758 of SEQ ID NO:2. In another example, the fragment lacks residues 679-697 (His motif) of SEQ ID NO:2. In yet another example, the fragment, lacks at least one residue of SEQ ID NO:2, the residue being selected from the group consisting of residue 661, 662, 663, 670, 671, 672, and 673. An HAAH fragment is an

15 HAAH polypeptide, the length of which is less than that of a full-length HAAH protein. The full-length HAAH protein is shown in Table 1.

        Diagnostic kits are also encompassed by the invention. For example, a kit for detecting a tumor cell contains an antibody, or fragment thereof, which binds to HAAH. The kit optionally contains a means for detecting binding of the antibody to the tumor

20 cell. For example, the kit contains a detectable marker, e.g., a nonradioactive marker such as Gd^{+++} or Fe^{++} or a radioactive compound. The kit may also contain instructions for use, a standard reagent for determining positive antibody binding, or a negative control for determining lack of antibody binding. The components are packaged together in a kit.

25   The assay format described herein is useful to generate temporal data used for prognosis of malignant disease. A method for prognosis of a malignant neoplasm of a mammal is carried out by (a) contacting a bodily fluid from the mammal with an

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antibody which binds to an HAAH polypeptide under conditions sufficient to form an antigen-antibody complex and detecting the antigen-antibody complex; (b) quantitating the amount of complex to determine the level of HAAH in the fluid; and (c) comparing the level of HAAH in the fluid with a normal control level of HAAH. An increasing

5   level of HAAH over time indicates a progressive worsening of the disease, and therefore, an adverse prognosis.

The invention also includes an antibody which binds to HAAH. The antibody preferably binds to a site in the carboxyterminal catalytic domain of HAAH. Alternatively, the antibody binds to an epitope that is exposed on the surface of the cell.

10   The antibody is a polyclonal antisera or monoclonal antibody. The invention encompasses not only an intact monoclonal antibody, but also an immunologically-active antibody fragment, e. g. , a Fab or (Fab)$_2$ fragment; an engineered single chain Fv molecule; or a chimeric molecule, e.g., an antibody which contains the binding specificity of one antibody, e.g., of murine origin, and the remaining portions of another antibody,

15   e.g., of human origin. Preferably the antibody is a monoclonal antibody such as FB50, 5C7, 5E9, 19B, 48A, 74A, 78A, 86A, HA238A, HA221, HA 239, HA241, HA329, or HA355. Antibodies which bind to the same epitopes as those monoclonal antibodies are also within the invention.

An HAAH-specific intrabody is a recombinant single chain HAAH-specific

20   antibody that is expressed inside a target cell, e.g., tumor cell. Such an intrabody binds to endogenous intracellular HAAH and inhibits HAAH enzymatic activity or prevents HAAH from binding to an intracellular ligand. HAAH-specific intrabodies inhibit intracellular signal transduction, and as a result, inhibit growth of tumors which overexpress HAAH.

25   A kit for diagnosis of a tumor in a mammal contains an HAAH-specific antibody. The diagnostic assay kit is preferentially formulated in a standard two-antibody binding format in which one HAAH-specific antibody captures HAAH in a

patient sample and another HAAH-specific antibody is used to detect captured HAAH. For example, the capture antibody is immobilized on a solid phase, e.g., an assay plate, an assay well, a nitrocellulose membrane, a bead, a dipstick, or a component of an elution column. The second antibody, i.e., the detection antibody, is typically tagged with a

5   detectable label such as a colorimetric agent or radioisotope.

Also within the invention is a method of inhibiting tumor growth in a mammal, which is carried out by administering to the mammal a compound which inhibits expression or enzymatic activity of HAAH. Preferably, the compound is substantially pure nucleic acid molecule such as an HAAH antisense DNA, the sequence

10   of which is complementary to a coding sequence of HAAH. Expression of HAAH is inhibited by contacting mammalian cells, e.g., tumor cells, with HAAH antisense DNA or RNA, e.g., a synthetic HAAH antisense oligonucleotide. The sequence of the antisense is complementary to a coding or noncoding region of a HAAH gene. For example, the sequence is complementary to a nucleotide sequence in the 5' untranslated

15   region of a HAAH gene. Examples of HAAH antisense oligonucleotides which inhibit HAAH expression in mammalian cells include oligonucleotides containing SEQ ID NO:10, 11, or 12. An HAAH antisense nucleic acid is introduced into glioblastoma cells or other tumor cells which overexpress HAAH. Binding of the antisense nucleic acid to an HAAH transcript in the target cell results in a reduction in HAAH production by the

20   cell. By the term "antisense nucleic acid" is meant a nucleic acid (RNA or DNA) which is complementary to a portion of an mRNA, and which hybridizes to and prevents translation of the mRNA. Preferably, the antisense DNA is complementary to the 5' regulatory sequence or the 5' portion of the coding sequence of HAAH mRNA (e.g., a sequence encoding a signal peptide or a sequence within exon 1 of the HAAH gene).

25   Standard techniques of introducing antisense DNA into the cell may be used, including those in which antisense DNA is a template from which an antisense RNA is transcribed. The method is to treat tumors in which expression of HAAH is upregulated, e.g., as a

result of malignant transformation of the cells. The length of the oligonucleotide is at least 10 nucleotides and may be as long as the naturally-occurring HAAH transcript. Preferably, the length is between 10 and 50 nucleotides, inclusive. More preferably, the length is between 10 and 20 nucleotides, inclusive.

5   By "substantially pure DNA or RNA" is meant that the nucleic acid is free of the genes which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank a HAAH gene. The term therefore includes, for example, a recombinant nucleic acid which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a procaryote or

10   eucaryote at a site other than its natural site; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant nucleic acid which is part of a hybrid gene encoding additional polypeptide sequence such as a nucleic acid encoding an chimeric polypeptide, e.g., one encoding an antibody fragment linked to

15   a cytotoxic polypeptide. Alternatively, HAAH expression is inhibited by administering a ribozyme or a compound which inhibits binding of Fos or Jun to an HAAH promoter sequence.

Compounds, which inhibit an enzymatic activity of HAAH, are useful to inhibit tumor growth in a mammal. By enzymatic activity of HAAH is meant

20   hydroxylation of an epidermal growth factor (EGF)-like domain of a polypeptide. For example an EGF-like domain has the consensus sequence $CX_7CX_4CX_{10}CXCX_8C$ (SEQ ID NO:1). HAAH hydroxylase activity is inhibited intracellularly. For example, a dominant negative mutant of HAAH (or a nucleic acid encoding such a mutant) is administered. The dominant negative HAAH mutant contains a mutation which changes

25   a ferrous iron binding site from histidine of a naturally-occurring HAAH sequence to a non-iron-binding amino acid, thereby abolishing the hydroxylase activity of HAAH. The histidine to be mutated, e.g., deleted or substituted, is located in the carboxyterminal

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catalytic domain of HAAH. For example, the mutation is located between amino acids 650-700 (such as the His motif, underlined sequence of SEQ ID NO:2) the native HAAH sequence. For example, the mutation is at residues 671, 675, 679, or 690 of SEQ ID NO:2. An HAAH-specific intrabody is also useful to bind to HAAH and inhibit

5 intracellular HAAH enzymatic activity, e.g., by binding to an epitope in the catalytic domain of HAAH. Other compounds such as L-mimosine or hydroxypyridone are administered directly into a tumor site or systemically to inhibit HAAH hydroxylase activity.

<div align="center">Table 1: Amino acid sequence of HAAH</div>

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10   MAQRKNAKSS  GNSSSSGSGS  GSTSAGSSSP  GARRETKHGG  HKNGRKGGLS  GTSFFTWFMV  61
     IALLGVWTSV  AVVWFDLVDY  EEVLGKLGIY  DADGDGDFDV  DDAKVLLGLK  ERSTSEPAVP  121
     PEEAEPHTEP  EEQVPVEAEP  QNIEDEAKEQ  IQSLLHEMVH  AEHVEGEDLQ  QEDGPTGEPQ  181
     QEDDEFLMAT  DVDDRFETLE  PEVSHEETEH  SYHVEETVSQ  DCNQDMEEMM  SEQENPDSSE  241
     PVVEDERLHH  DTDDVTYQVY  EEQAVYEPLE  NEGIEITEVT  APPEDNPVED  SQVIVEEVSI  301
15   FPVEEQQEVP  PETNRKTDDP  EQKAKVKKKK  PKLLNKFDKT  IKAELDAAEK  LRKRGKIEEA  361
     VNAFKELVRK  YPQSPRARYG  KAQCEDDLAE  KRRSNEVLRG  AIETYQEVAS  LPDVPADLLK  421
     LSLKRRSDRQ  QFLGHMRGSL  LTLQRLVQLF  PNDTSLKNDL  GVGYLLIGDN  DNAKKVYEEV  481
     LSVTPNDGFA  KVHYGFILKA  QNKIAESIPY  LKEGIESGDP  GTDDGRFYFH  LGDAMQRVGN  541
     KEAYKWYELG  HKRGHFASVW  QRSLYNVNGL  KAQPWWTPKE  TGYTELVKSL  ERNWKLIRDE  601
20   GLAVMDKAKG  LFLPEDENLR  EKGDWSQFTL  WQQGRRNENA  CKGAPKTCTL  LEKFPETTGC  661
     RRGQIKYSIM  HPGTHVWPHT  GPTNCRLRMH  LGLVIPKEGC  KIRCANETRT  WEEGKVLIFD  721
     DSFEHEVWQD  ASSFRLIFIV  DVWHPELTPQ  QRRSLPAI (SEQ ID NO:2; GENBANK Accession No.
     S83325; His motif is underlined; conserved sequences within the catalytic domain are designated by bold
     type)
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25   For example, a compound which inhibits HAAH hydroxylation is a polypeptide that binds a HAAH ligand but does not transduce an intracellular signal or an polypeptide which contains a mutation in the catalytic site of HAAH. Such a polypeptide contains an amino acid sequence that is at least 50% identical to a naturally-occurring HAAH amino acid sequence or a fragment thereof and which has the ability to inhibit

30 HAAH hydroxylation of substrates containing an EGF-like repeat sequence. More preferably, the polypeptide contains an amino acid sequence that is at least 75%, more preferably at least 85%, more preferably at least 95% identical to SEQ ID NO:2.

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A substantially pure HAAH polypeptide or HAAH-derived polypeptide such as a mutated HAAH polypeptide is preferably obtained by expression of a recombinant nucleic acid encoding the polypeptide or by chemically synthesizing the protein. A polypeptide or protein is substantially pure when it is separated from those
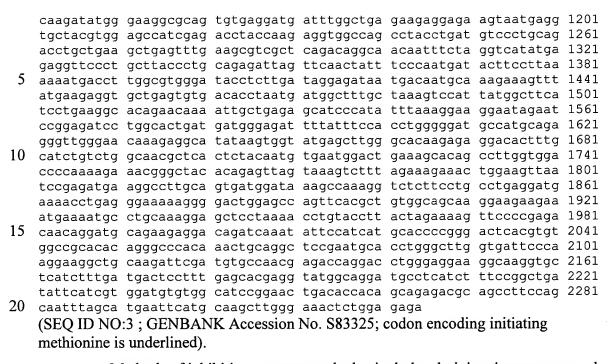
5   contaminants which accompany it in its natural state (proteins and other naturally-occurring organic molecules). Typically, the polypeptide is substantially pure when it constitutes at least 60%, by weight, of the protein in the preparation. Preferably, the protein in the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, HAAH. Purity is measured by any appropriate

10   method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis. Accordingly, substantially pure polypeptides include recombinant polypeptides derived from a eucaryote but produced in *E. coli* or another procaryote, or in a eucaryote other than that from which the polypeptide was originally derived.

Nucleic acid molecules which encode such HAAH or HAAH-derived

15   polypeptides are also within the invention.

Table 2: HAAH cDNA sequence

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     cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 61
     gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccgg agagagacaa 121
     agcatggagg acacaagaat gggaggaaag gcggactctc gggaacttca ttcttcacgt 181
20   ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 241
     ttgttgacta tgaggaagtt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 301
     attttgatgt ggatgatgcc aaagttttat taggacttaa agagagatct acttcagagc 361
     cagcagtccc gccagaagag gctgagccac acactgagcc cgaggagcag gttcctgtgg 421
     aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtcc cttctccatg 481
25   aaatggtaca cgcagaacat gttgagggag aagacttgca acaagaagat ggacccacag 541
     gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 601
     agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 661
     cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 721
     attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 781
30   accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 841
     cagaagtaac tgctcccect gaggataatc ctgtagaaga ttcacaggta attgtagaag 901
     aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 961
     cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1021
     ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1081
35   ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1141
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     caagatatgg gaaggcgcag tgtgaggatg atttggctga gaagaggaga agtaatgagg 1201
     tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1261
     acctgctgaa gctgagtttg aagcgtcgct cagacaggca acaatttcta ggtcatatga 1321
     gaggttccct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1381
   5 aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1441
     atgaagaggt gctgagtgtg acacctaatg atggctttgc taaagtccat tatggcttca 1501
     tcctgaaggc acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1561
     ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1621
     gggttgggaa caaagaggca tataagtggt atgagcttgg gcacaagaga ggacactttg 1681
  10 catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttggtgga 1741
     ccccaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaagttaa 1801
     tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1861
     aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1921
     atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1981
  15 caacaggatg cagaagagga cagatcaaat attccatcat gcaccccggg actcacgtgt 2041
     ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2101
     aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaaggtgc 2161
     tcatctttga tgactccttt gagcacgagg tatggcagga tgcctcatct ttccggctga 2221
     tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2281
  20 caatttagca tgaattcatg caagcttggg aaactctgga gaga
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(SEQ ID NO:3 ; GENBANK Accession No. S83325; codon encoding initiating methionine is underlined).

Methods of inhibiting tumor growth also include administering a compound which inhibits HAAH hydroxylation of a NOTCH polypeptide. For example, the compound inhibits hydroxylation of an EGF-like cysteine-rich repeat sequence in a NOTCH polypeptide, e.g., one containing the consensus sequence CDXXXCXXKXGNGXCDXXCNNAACXXDGXDC (SEQ ID NO:4). Polypeptides containing an EGF-like cysteine-rich repeat sequence are administered to block hydroxylation of endogenous NOTCH.

Growth of a tumor which overexpresses HAAH is also inhibited by administering a compound which inhibits signal transduction through the insulin receptor substrate (IRS) signal transduction pathway. Preferably the compound inhibits IRS phosphorylation. For example, the compound is a peptide or non-peptide compound which binds to and inhibits phosphorylation at residues 46, 465, 551, 612, 632, 662, 732, 941, 989, or 1012 of SEQ ID NO:5 . Compounds include polypeptides such those which block an IRS phosphorylation site such as a Glu/Tyr site. Antibodies such as those which

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bind to a carboxyterminal domain of IRS containing a phosphorylation site block IRS phosphorylation, and as a consequence, signal transduction along the pathway. Inhibition of IRS phosphorylation in turn leads to inhibition of cell proliferation. Other compounds which inhibit IRS phosphorylation include vitamin D analogue EB1089 and Wortmannin.

5   HAAH-overproducing tumor cells were shown to express HAAH both intracellularly and on the surface of the tumor cell. Accordingly, a method of killing a tumor cell is carried out by contacting such a tumor cell with a cytotoxic agent linked to an HAAH-specific antibody. The HAAH-specific antibody (antibody fragment, or ligand which binds to extracellular HAAH) directs the chimeric polypeptide to the surface of the

10 tumor cell allowing the cytotoxic agent to damage or kill the tumor cell to which the antibody is bound. The monoclonal antibody binds to an epitope of HAAH such as an epitope exposed on the surface of the cell or in the catalytic site of HAAH. The cytotoxic composition preferentially kills tumor cells compared to non-tumor cell.

          Screening methods to identify anti-tumor agents which inhibit the growth of

15 tumors which overexpress HAAH are also within the invention. A screening method used to determine whether a candidate compound inhibits HAAH enzymatic activity includes the following steps: (a) providing a HAAH polypeptide, e.g., a polypeptide which contains the carboxyterminal catalytic site of HAAH; (b) providing a polypeptide comprising an EGF-like domain; (c) contacting the HAAH polypeptide or the EGF-like

20 polypeptide with the candidate compound; and (d) determining hydroxylation of the EGF-like polypeptide of step (b). A decrease in hydroxylation in the presence of the candidate compound compared to that in the absence of the compound indicates that the compound inhibits HAAH hydroxylation of EGF-like domains in proteins such as NOTCH.

25   Anti-tumor agents which inhibit HAAH activation of NOTCH are identified by (a) providing a cell expressing HAAH; (b) contacting the cell with a candidate compound; and (c) measuring translocation of activated NOTCH to the nucleus of the

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cell. Translocation is measured by using a reagent such as an antibody which binds to a 110 kDa activation fragment of NOTCH. A decrease in translocation in the presence of the candidate compound compared to that in the absence of the compound indicates that the compound inhibits HAAH activation of NOTCH, thereby inhibiting NOTCH-

5   mediated signal transduction and proliferation of HAAH-overexpressing tumor cells.

Nucleotide and amino acid comparisons described herein were carried out using the Lasergene software package (DNASTAR, Inc., Madison, WI). The MegAlign module used was the Clustal V method (Higgins et al., 1989, CABIOS 5(2):151-153). The parameter used were gap penalty 10, gap length penalty 10.

10   Hybridization is carried out using standard techniques, such as those described in Ausubel *et al.* (*Current Protocols in Molecular Biology*, John Wiley & Sons, 1989). "High stringency" refers to nucleic acid hybridization and wash conditions characterized by high temperature and low salt concentration, *e.g.*, wash conditions of 65°C at a salt concentration of 0.1 X SSC. "Low" to "moderate" stringency refers to DNA

15   hybridization and wash conditions characterized by low temperature and high salt concentration, *e.g.*, wash conditions of less than 60°C at a salt concentration of 1.0 X SSC. For example, high stringency conditions include hybridization at 42°C in the presence of 50% formamide; a first wash at 65°C in the presence of 2 X SSC and 1% SDS; followed by a second wash at 65°C in the presence of 0.1% x SSC. Lower

20   stringency conditions suitable for detecting DNA sequences having about 50% sequence identity to an HAAH gene sequence are detected by, for example, hybridization at about 42°C in the absence of formamide; a first wash at 42°C, 6 X SSC, and 1% SDS; and a second wash at 50°C, 6 X SSC, and 1% SDS.

Other features and advantages of the invention will be apparent from the

25   following description of the preferred embodiments thereof, and from the claims.

Fig. 1 is a bar graph showing colony formation induced by transient transfection of NIH-3T3 cells with various aspartyl (asparaginyl) beta-hydroxylase (AAH) cDNAs. Colony formation was induced by transient transfection with 10 µg

5 DNA. In contrast, the mutant murine AAH construct without enzymatic activity has no transforming activity. The data is presented as mean number of transformed foci ± SEM.

Fig. 2 is a bar graph showing the results of a densitometric analysis of a Western blot assay of proteins produced by various murine AAH stably transfected cell clones. In clones 7 and 18, there was a modest increase in HAAH gene expression, while

10 the overexpression was to a lesser degree in clone 16.

Figs. 3A-B are bar graphs showing colony formation in soft agar exhibited by HAAH stably transfected clones compared to HAAH enzymatic activity. Fig. 3A shows a measurement of murine AAH enzymatic activity in clones 7, 16 and 18, and Fig. 3B shows colony formation exhibited by clones 7, 16 and 18. Data is presented as mean

15 number of colonies 10 days after plating ± SEM. All three clones with modest increases in HAAH enzymatic activity, that correlated with protein expression, exhibited anchorage independent growth.

Fig. 4 is a bar graph showing tumor formation in nude mice injected with transfected clones overexpressing murine AAH. Tumor growth was assessed after

20 30 days. Mean tumor weight observed in mice injected with clones 7, 16 and 18 as compared to mock DNA transfected clone. All animals, which were injected with clones overexpressing HAAH, developed tumors.

Figs. 5A-D are bar graphs showing increased AAH expression in PNET2 (Fig. 5A, 5C) and SH-Sy5y (Fig. 5B) cells treated with retinoic acid (Figs. 5A, 5B) or phorbol

25 ester myristate (PMA; Fig. 5C) to induce neurite outgrowth as occurs during tumor cell invasion. The cells were treated with 10 µM retinoic acid or 100 nM PMA for 0, 1, 2, 3, 4, or 7 days. Cell lysates were analyzed by Western blot analysis using an HAAH-

specific monoclonal antibody to detect the 85 kDa AAH protein. The levels of immunoreactivity were measured by volume densitometry (arbitrary units). The graphs indicate the mean ± S.D. of results obtained from three separate experiments. In Fig. 5D, PNET2 cells were treated for 24 hours with sub-lethal concentrations of H_2O_2 to induce

5   neurite retraction. Viability of greater than 90% of the cells was demonstrated by Trypan blue dye exclusion. Similar results were obtained for SH-Sy5y cells.

Fig. 6 is a bar graph showing the effects of AAH over-expression on the levels of anti-apoptosis (Bcl-2), cell cycle-mitotic inhibitor (p16 and p21/Waf1), and proliferation (proliferating cell nuclear antigen; PCNA) molecules. PNET2 neuronal

10   cells were stably transfected with the full-length human cDNA encoding AAH (pHAAH) or empty vector (pcDNA). AAH gene expression was under control of a CMV promoter. Western blot analysis was performed with cell lysates prepared from cultures that were 70 to 80 percent confluent. Protein loading was equivalent in each lane. Replicate blots were probed with the different antibodies. Bar graphs depict the mean S.D.'s of protein

15   expression levels measured in three experiments. All differences are statistically significant by Student T-test analysis (P<0.01-P<0.001).

Fig. 7 is a diagram of showing the components of the IRS-1 signal transduction pathway.

Fig. 8 is a line graph showing growth curves generated in cells expressing the

20   antisense HAAH compared to controls expressing GFP.

Fig. 9 is a diagram of the functional domains of the hIRS-1 protein and structural organization of the point mutants. All mutant and "wild type" hIRS-1 proteins construct contain a FLAG (F) epitope (DYKDDDDK; SEQ ID NO:7) at the C-terminus. PH and PTB indicate pleckstrin homology and phosphotyrosine binding, regions,

25   respectively.

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Fig. 10 is a diagram showing AAH cDNA and the location at which antisense oligonucleotides bind. The locations shown are relative to the AUG start site of the AAH cDNA.

Fig. 11 is a photograph of an electrophoretic gel showing inhibition of AAH gene expression by antisense oligonucleotide DNA molecules.

Fig. 12 is a line graph showing AAH antisense oligonucleotide binding in neuroblastoma cells.

Fig. 13 is a bar graph showing inhibition of AAH gene expression as a result of AAH antisense oligonucleotide delivery into neuroblastoma cells.

Fig. 14A is a photograph of a Western blot assay expression of NOTCH proteins.

Fig. 14B is a photograph of an electrophoretic gel showing Hes-1 gene expression as measured by reverse transcriptase - polymerase chain reaction (RT-PCR).

Fig. 14C is a photograph of a Western blot assay showing expression of NOTCH-1 and Jagged-1 under conditions in which IRS-1 signalling is reduced.

Detailed Description

HAAH is a protein belonging to the alpha-ketoglutarate dependent dioxygenase family of prolyl and lysyl hydroxylases which play a key role in collagen biosynthesis. This molecule hydroxylates aspartic acid or asparagine residues in EGF-like domains of several proteins in the presence of ferrous iron. These EGF-like domains contain conserved motifs, that form repetitive sequences in proteins such as clotting factors, extracellular matrix proteins, LDL receptor, NOTCH homologues, or NOTCH ligand homologues.

The alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginyl) beta-hydroxylase (AAH) specifically hydroxylates one aspartic or asparagine residue in EGF-like domains of various proteins. The 4.3-kb cDNA encoding the human AspH (hAspH) hybridizes with 2.6 kb and 4.3 kb transcripts in transformed cells, and the

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deduced amino acid sequence of the larger transcript encodes an protein of about 85 kDa. Both *in vitro* transcription and translation and Western blot analysis also demonstrate a 56-kDa protein that may result from posttranslational cleavage of the catalytic C-terminus.

5   A physiological function of AAH is the post-translational beta-hydroxylation of aspartic acid in vitamin K-dependent coagulation proteins. However, the abundant expression of AAH in several malignant neoplasms, and low levels of AAH in many normal cells indicate a role for this enzyme in malignancy. The AAH gene is also highly expressed in cytotrophoblasts, but not syncytiotrophoblasts of the placenta.

10 Cytotrophoblasts are invasive cells that mediate placental implantation. The increased levels of AAH expression in human cholangiocarcinomas, hepatocellular carcinomas, colon cancers, and breast carcinomas were primarily associated with invasive or metastatic lesions. Moreover, overexpression of AAH does not strictly reflect increased DNA synthesis and cellular proliferation since high levels of AAH immunoreactivity

15 were observed in 100 percent of cholangiocarcinomas, but not in human or experimental disease processes associated with regeneration or nonneoplastic proliferation of bile ducts. AAH overexpression and attendant high levels of beta hydroxylase activity lead to invasive growth of transformed neoplastic cells. Detection of an increase in HAAH expression is useful for early and reliable diagnosis of the cancer types which have now

20 been characterized as overexpressing this gene product.

Diagnosis of malignant tumors

          HAAH is overexpressed in many tumors of endodermal origin and in at least 95% of CNS tumors compared to normal noncancerous cells. An increase in HAAH gene product in a patient-derived tissue sample (e.g., solid tissue or bodily fluid) is

25 carried out using standard methods, e.g., by Western blot assays or a quantitative assay such as ELISA. For example, a standard competitive ELISA format using an HAAH-specific antibody is used to quantify patient HAAH levels. Alternatively, a sandwich

ELISA using a first antibody as the capture antibody and a second HAAH-specific antibody as a detection antibody is used.

Methods of detecting HAAH include contacting a component of a bodily fluid with an HAAH-specific antibody bound to solid matrix, e.g., microtiter plate, bead,
5   dipstick. For example, the solid matrix is dipped into a patient-derived sample of a bodily fluid, washed, and the solid matrix is contacted with a reagent to detect the presence of immune complexes present on the solid matrix.

Proteins in a test sample are immobilized on (e.g., bound to) a solid matrix. Methods and means for covalently or noncovalently binding proteins to solid matrices are
10   known in the art. The nature of the solid surface may vary depending upon the assay format. For assays carried out in microtiter wells, the solid surface is the wall of the microtiter well or cup. For assays using beads, the solid surface is the surface of the bead. In assays using a dipstick (i.e., a solid body made from a porous or fibrous material such as fabric or paper) the surface is the surface of the material from which the dipstick
15   is made. Examples of useful solid supports include nitrocellulose (e.g., in membrane or microtiter well form), polyvinyl chloride (e.g., in sheets or microtiter wells), polystyrene latex (e.g., in beads or microtiter plates, polyvinylidine fluoride (known as IMMULON™), diazotized paper, nylon membranes, activated beads, and Protein A beads. The solid support containing the antibody is typically washed after contacting it
20   with the test sample, and prior to detection of bound immune complexes. Incubation of the antibody with the test sample is followed by detection of immune complexes by a detectable label. For example, the label is enzymatic, fluorescent, chemiluminescent, radioactive, or a dye. Assays which amplify the signals from the immune complex are also known in the art, e.g., assays which utilize biotin and avidin.
25   An HAAH-detection reagent, e.g., an antibody, is packaged in the form of a kit, which contains one or more HAAH-specific antibodies, control formulations

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(positive and/or negative), and/or a detectable label. The assay may be in the form of a standard two-antibody sandwich assay format known in the art.

Production of HAAH-specific antibodies

Anti-HAAH antibodies were obtained by techniques well known in the art.

5 Such antibodies are polyclonal or monoclonal. Polyclonal antibodies were obtained using standard methods, e.g., by the methods described in Ghose et al., Methods in Enzymology, Vol. 93, 326-327, 1983. An HAAH polypeptide, or an antigenic fragment thereof, was used as the immunogen to stimulate the production of polyclonal antibodies in the antisera of rabbits, goats, sheep, or rodents. Antigenic polypeptides for production

10 of both polyclonal and monoclonal antibodies useful as immunogens include polypeptides which contain an HAAH catalytic domain. For example, the immunogenic polypeptide is the full-length mature HAAH protein or an HAAH fragment containing the carboxyterminal catalytic domain e.g., an HAAH polypeptide containing the His motif of SEQ ID NO:2.

15 Antibodies which bind to the same epitopes as those antibodies disclosed herein are identified using standard methods, e.g., competitive binding assays, known in the art.

Monoclonal antibodies were obtained by standard techniques. Ten µg of purified recombinant HAAH polypeptide was administered to mice intraperitoneally in

20 complete Freund's adjuvant, followed by a single boost intravenously (into the tail vein) 3-5 months after the initial inoculation. Antibody-producing hybridomas were made using standard methods. To identify those hybridomas producing antibodies that were highly specific for an HAAH polypeptide, hybridomas were screened using the same polypeptide immunogen used to immunize. Those antibodies which were identified as

25 having HAAH-binding activity are also screened for the ability to inhibit HAAH catalytic activity using the enzymatic assays described below. Preferably, the antibody has a

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binding affinity of at least about 10^8 liters/mole and more preferably, an affinity of at least about 10^9 liters/mole.

Monoclonal antibodies are humanized by methods known in the art, e.g, MAbs with a desired binding specificity can be commercially humanized (Scotgene,

5   Scotland; Oxford Molecular, Palo Alto, CA).

HAAH-specific intrabodies are produced as follows. Following identification of a hybridoma producing a suitable monoclonal antibody, DNA encoding the antibody is cloned. DNA encoding a single chain HAAH-specific antibody in which heavy and light chain variable domains are separated by a flexible linker peptide is cloned into an

10   expression vector using known methods (e.g., Marasco et al., 1993, Proc. Natl. Acad. Sci. USA 90:7889-7893 and Marasco et al., 1997, Gene Therapy 4:11-15). Such constructs are introduced into cells, e.g., using standard gene delivery techniques for intracellular production of the antibodies. Intracellular antibodies, i.e., intrabodies, are used to inhibit signal transduction by HAAH. Intrabodies which bind to a

15   carboxyterminal catalytic domain of HAAH inhibit the ability of HAAH to hydroxylate EGF-like target sequences.

Methods of linking HAAH-specific antibodies (or fragments thereof) which bind to cell surface exposed epitopes of HAAH on the surface of a tumor cell are linked to known cytotoxic agents, e.g, ricin or diptheria toxin, using known methods.

20   Deposit of Biological Materials

Under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure, hybridoma FB501 (which produces monoclonal antibody FB50), hybridoma HA386A (which produces monoclonal antibody 86A), hybridoma HA15C7A (which produces monoclonal antibody

25   5C7), and hybridoma HA219B (which produces monoclonal antibody 19B) were deposited on May 17, 2001, with the American Type Culture Collection (ATCC) of 10801 University Boulevard, Manassas, Va. 20110-2209 USA..

20

Applicants' assignee represents that the ATCC is a depository affording permanence of

the deposit and ready accessibility thereto by the public if a patent is granted. All

5   restrictions on the availability to the public of the material so deposited will be

irrevocably removed upon the granting of a patent. The material will be available during

the pendency of the patent application to one determined by the Commissioner to be

entitled thereto under 37 CFR 1.14 and 35 U.S.C. 122. The deposited material will be

maintained with all the care necessary to keep it viable and uncontaminated for a period

10   of at least five years after the most recent request for the furnishing of a sample of the

deposited plasmid, and in any case, for a period of at least thirty (30) years after the date

of deposit or for the enforceable life of the patent, whichever period is longer.

Applicant's assignee acknowledges its duty to replace the deposit should the depository

be unable to furnish a sample when requested due to the condition of the deposit.

15   Methods of treating malignant tumors

Patients with tumors characterized as overexpressing HAAH as such tumors

of endodermal origin or CNS tumors are treated by administering HAAH antisense

nucleic acids.

Antisense therapy is used to inhibit expression of HAAH in patients suffering

20   from hepatocellular carcinomas, cholangiocarcinomas, glioblastomas and

neuroblastomas. For example, an HAAH antisense strand (either RNA or DNA) is

directly introduced into the cells in a form that is capable of binding to the mRNA

transcripts. Alternatively, a vector containing a sequence which, which once within the

target cells, is transcribed into the appropriate antisense mRNA, may be administered.

25   Antisense nucleic acids which hybridize to target mRNA decrease or inhibit production

of the polypeptide product encoded by a gene by associating with the normally single-

stranded mRNA transcript, thereby interfering with translation and thus, expression of the

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protein. For example, DNA containing a promoter, e.g., a tissue-specific or tumor specific promoter, is operably linked to a DNA sequence (an antisense template), which is transcribed into an antisense RNA. By "operably linked" is meant that a coding sequence and a regulatory sequence(s) (*i.e.*, a promoter) are connected in such a way as to

5 permit gene expression when the appropriate molecules (*e.g.*, transcriptional activator proteins) are bound to the regulatory sequence(s).

Oligonucleotides complementary to various portions of HAAH mRNA were tested *in vitro* for their ability to decrease production of HAAH in tumor cells (e.g., using the FOCUS hepatocellular carcinoma (HCC) cell line) according to standard methods. A

10 reduction in HAAH gene product in cells contacted with the candidate antisense composition compared to cells cultured in the absence of the candidate composition is detected using HAAH-specific antibodies or other detection strategies. Sequences which decrease production of HAAH in *in vitro* cell-based or cell-free assays are then be tested *in vivo* in rats or mice to confirm decreased HAAH production in animals with malignant

15 neoplasms.

Antisense therapy is carried out by administering to a patient an antisense nucleic acid by standard vectors and/or gene delivery systems. Suitable gene delivery systems may include liposomes, receptor-mediated delivery systems, naked DNA, and viral vectors such as herpes viruses, retroviruses, adenoviruses and adeno-associated

20 viruses, among others. A reduction in HAAH production results in a decrease in signal transduction via the IRS signal transduction pathway. A therapeutic nucleic acid composition is formulated in a pharmaceutically acceptable carrier. The therapeutic composition may also include a gene delivery system as described above. Pharmaceutically acceptable carriers are biologically compatible vehicles which are

25 suitable for administration to an animal: e.g., physiological saline. A therapeutically effective amount of a compound is an amount which is capable of producing a medically

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desirable result such as reduced production of an HAAH gene product or a reduction in tumor growth in a treated animal.

Parenteral administration, such as intravenous, subcutaneous, intramuscular, and intraperitoneal delivery routes, may be used to deliver nucleic acids or HAAH-
5 inhibitory peptides or non-peptide compounds. For treatment of CNS tumors, direct infusion into cerebrospinal fluid is useful. The blood-brain barrier may be compromised in cancer patients, allowing systemically administered drugs to pass through the barrier into the CNS. Liposome formulations of therapeutic compounds may also facilitate passage across the blood-brain barrier.

10 Dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular nucleic acid to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Dosage for intravenous administration of nucleic acids is from approximately 10^6 to 10^{22} copies of the nucleic acid molecule.

15 Ribozyme therapy is also be used to inhibit HAAH gene expression in cancer patients. Ribozymes bind to specific mRNA and then cut it at a predetermined cleavage point, thereby destroying the transcript. These RNA molecules are used to inhibit expression of the HAAH gene according to methods known in the art (Sullivan et al., 1994, J. Invest. Derm. 103:85S-89S; Czubayko et al., 1994, J. Biol. Chem. 269:21358-
20 21363; Mahieu et al, 1994, Blood 84:3758-65; Kobayashi et al. 1994, Cancer Res. 54:1271-1275).

HAAH-specific antibodies inhibit tumor cell growth

HAAH-specific antibodies inhibit the proliferation of tumor cells in culture. Two different HAAH-specific antibodies, FB-50 and 5C7, were tested. Tumor cells (a
25 heptatocarcinoma cell line, a lung carcinoma cell line, and a breast carcinoma cell line) were seeded in a 96 well plate and incubated with varying concentrations of antibody for 48 hours. The cells were fixed with acetone. Cell growth was monitored using a

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sulforhodamine B dye binding assay. The data indicated a reduction in cell viability and proliferation in the presence of FB50 compared to in its absence.

Passive Immunization

The HAAH-specific antibodies described herein are used to inhibit the growth of

5　a tumor cell or kill the tumor cell.

Purified antibody preparations (e.g., a purified monoclonal antibody, an antibody fragment, or single chain antibody) is administered to an individual diagnosed with a tumor or at risk of developing a tumor. The antibody preparations are administered using methods known in the art of passive immunization, e.g., intravenously or intramuscularly.

10　The antibodies used in the methods described herein are formulated in a physiologically-acceptable excipient. Such excipients, e.g., physiological saline, are known in the art.

The antibody is preferably a high-affinity antibody, e.g., an IgG-class antibody or fragment or single chain thereof. Alternatively, the antibody is an IgM isotype. Antibodies are monoclonal, e.g., a murine monoclonal antibody or fragment thereof, or a

15　murine monoclonal antibody, which has been humanized. The antibody is a human monoclonal antibody. The affinity of a given monoclonal antibody is further increased using known methods, e.g., by selecting for increasingly higher binding capacity (e.g., according to the method described in Boder et al., 2000, Proc. Natl. Acad. Sci. U.S.A. 97:10701-10705). Optionally, the antibody, antibody fragment, or high affinity single

20　chain antibody is conjugated to a toxic moiety prior to administration. Toxic moities suitable for conjugation include ricin, Psuedomonas toxin, Diptheria toxin as well as radioisotopes and chemotherapeutic agents known in the art. Such antibody toxins damage or kill a tumor cell upon binding to the tumor cell or upon internalization into the cytoplasm of the tumor cell.

25　Antibody preparations or antibody-toxin preparations are administered at doses of approximately 0.01-2 mL/kg of body weight. Doses are readministered weekly or monthly as necessary to reduce tumor load in a treated individual.

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Active Immunization

Active vaccination is the process of inducing an animal to respond to an antigen. During vaccination, cells, which recognize the antigen (B cells or cytotoxic T cells), are clonally expanded. In addition, the population of helper T cells specific for the antigen

5 also increase. Vaccination also involves specialized antigen presenting cells, which can process the antigen and display it in a form which can stimulate one of the two pathways. Antigen recognition followed by immune cell expansion and activation leads to the production of antigen-specific antibodies and antigen-specific cellular immune responses. Successful immunization is indicated by an increase in the level of HAAH-specific

10 antibody titer in serum of an immunized individual compared to the level prior to immunization. Preferably, the HAAH-specific antibody titer is at least 10%, more preferably at least 50%, more preferably at least 100%, and most preferably 200% greater than the titer prior to immunization.

An individual is immunized with an AAH (e.g., HAAH) polypeptide or a

15 polynucleotide encoding the peptide. For example, a human patient is immunized with full-length 52 kDa HAAH. Standard adjuvant formulations may be simultaneously administered to enhance immunogenicity of the immunizing polypeptide. Alternatively, shorter polypeptides, e.g., immunogenic fragments of HAAH, are used. For example, a polypeptide contains an extracellular catalytic domain of HAAH (e.g., amino acids 650-

20 700 of SEQ ID NO:2). Other immunogenic fragments of HAAH include a fragment contains a binding site for alpha-ketoglutarate, a fragment that lacks a binding site for alpha-ketoglutarate, one which contains a calcium binding site, and one which lacks a binding site for an EGF-like polypeptide.

DNA vaccine

25 In addition to standard active vaccination using a peptide antigen, DNA vaccination is used to generate an immune response to HAAH, and in turn to tumor cells, which overexpress HAAH. Although HAAH is overexpressed on malignant cells, an

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effective immune response is not made by the patient because tumor cells lack appropriate accessory molecules for antigen presentation. The DNA vaccines described herein result in generation of a humoral as well as cellular immunity specific for HAAH (and cells expressing HAAH on their cell surface). For example, not only is an HAAH-

5   specific antibody produced in the immunized individual, HAAH-specific cytotoxic T cells are generated. HAAH-specific cytotoxic T cells kill tumor cells, thereby reducing tumor load in the immunized individual.

A polynucleotide encoding an AAH polypeptide (full-length or an immunogenic fragment of AAH) is introduced into an individual by known methods, e.g., particle

10   bombardment or direct injection via needle. Typically, the antigen (or DNA encoding the antigen) is delivered intramuscularly. The antigen is also directly injected into other tissues, e.g., tumor sites. DNA is taken up by cells at the point of injection. The cell produces proteins, and the proteins stimulate the immune system of the immunized individual resulting, e.g., in generation of an HAAH-specific antibody. Cellular

15   immunity, e.g., cytotoxic T cells, are also generated.

An effective DNA or mRNA dosage is generally be in the range of from about 0.05 micrograms/kg to about 50 mg/kg, usually about 0.005-5 mg/kg of body weight, e.g., 0.5 to 5 mg/kg. The DNA to be administered is naked (in the absence of transfection-facilitating substances) or complexed with compounds, which enhance

20   cellular uptake of the polynucleotide (e.g., charged lipids, lipid complexes or liposomes). For example, the polynucleotide is administered with Lipofectin^{TM} or precipitating agents such as $CaPO_4$. The transfected cells, e.g., non-proliferating muscle cells, produce the recombinant antigenic polypeptide for at least one month and up to several months, e.g. 3-6 months. Alternatively, transitory expression of a polypeptide is achieved by

25   introducing the polynucleotide construct into a tissue (e.g., non-muscular tissue or tumor tissue). In the latter case, cells of the tissue produce the polypeptide for a shorter period of time, e.g., several days (3-5 days and up to about 20 days). The level of protein or

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polypeptide expression by target cells is sufficient to induce production of HAAH-specific antibodies. The level of antibody production is measured using standard methods, e.g., evaluation of antibody titer in patient serum, before and after immunization.

5   The polynucleotides are administered by standard methods, such as by injection into the interstitial space of tissues such as muscles or skin, introduction into the circulation or into body cavities or by inhalation or insufflation. Polynucleotides are injected or otherwise delivered to the animal with a pharmaceutically acceptable liquid carrier, e.g., a liquid carrier, which is aqueous or partly aqueous. The polynucleotides are

10   associated with a liposome (e.g., a cationic or anionic liposome). The polynucleotide includes genetic information necessary for expression by a target cell, such as a promoters.

One advantage of DNA vaccination is that DNA vaccines can result in longer lasting production of the antigenic protein, thereby booster shots reducing or avoiding

15   booster immunizations.

In addition to inducing an immune response, e.g., an HAAH-specific antibody response, by vaccinating with DNA encoding an HAAH polypeptide, a polynucleotide encoding the antibody itself is introduced. An isolated polynucleotide encoding an HAAH-specific antibody, e.g., variable regions of the antibody, is introduced for

20   production of the antibody *in situ*. The antibody in turn exerts a therapeutic effect at the target site by binding a cell surface antigen, e.g., extracellular HAAH, or by binding to a catalytic domain of HAAH, to inhibit HAAH function.

In vivo diagnostic imaging

The antibodies (antibody fragments, and single chain antibodies) described herein

25   are useful to diagnose the presence of a tumor in tissues as well as bodily fluids. HAAH-specific antibodies are tagged with a detectable label such as a radioisotope or colorimeteric agent. The labeled antibody is administered to an individual at risk of

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developing cancer or an individual who has previously been diagnosed with cancer. For example, the antibodies are useful to diagnose metastases of a tumor, which has been surgically excised or treated by chemotherapeutic or radiotherapeutic methods. The sensitivity of the method is sufficient to detect micrometastases in tissues such as lymph

5   nodes. Early and sensitive diagnosis of tumors in this manner allows prompt therapeutic intervention.

The labeled antibody is administered to an individual using known methods, e.g., intravenously, or direct injection into solid or soft tissues. The antibody is allowed to distribute throughout the tissue or throughout the body for a period of approximately 1

10 hour to 72 hours. The whole body of the individual is then imaged using methods known in the art. Alternatively, a small portion of the body, e.g., a tissue site suspected of harboring a tumor, is imaged. An increase in antibody binding, as measured by an increase in detection of the label, over the level of baseline binding (to normal tissue) indicates the presence of a tumor at the site of binding.

15 Activation of NOTCH signaling

NOTCH signalling is activated in cells highly expressing AAH. Fig. 14A shows the presence of a 110 kDa NOTCH fragment as revealed by using Western blot. Overexpression of enzymatically active AAH is shown by a display of the 100 kDa cleaved, active NOTCH-1 (Lane 1, Mock DNA transfected clone; Lane 2, clones 7; and

20 Lane 3, clone18). In contrast, NOTCH-2 was not activated. There was enhanced expression of the full length Jagged ligand in clones expressing AAH as compared to the mock DNA transfected clone. Tubulin was used as internal control for protein loading.

Expression of the Hes-1, a known downstream effector gene, is activated by NOTCH signaling (Fig. 14B). Only AAH-expressing clones activate Notch expression

25 as a transcription factor and subsequently unregulates Hes-1 gene expression as revealed by competitive RT-PCR. Lower panel is an RT-PCR product of GAPDII that served as internal control. Fig. 14C shows expression of human NOTCH-1 (hNOTCH-1) and

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Jagged-1 where IRS-1 signaling is reduced by a dominant negative mutant (DhIRS-1). Such cells demonstrate downregulation AAH expression and demonstrate a parallel decrease in NOTCH-1 and Jagged levels by Western blot analysis. Tubulin was used as an internal control for protein loading.

5   Methods of identifying compounds that inhibit HAAH enzymatic activity

Aspartyl (asparaginyl) beta-hydroxylaseydroxylase (AAH) activity is measured *in vitro* or *in vivo*. For example, HAAH catalyzes posttranslational modification of β carbon of aspartyl and asparaginyl residues of EGF-like polypeptide domains. An assay to identify compounds which inhibit hydroxylase activity is carried
10   out by comparing the level of hydroxylation in an enzymatic reaction in which the candidate compound is present compared to a parallel reaction in the absence of the compound (or a predetermined control value). Standard hydroxylase assays carried out in a testtube are known in the art, e.g., Lavaissiere et al., 1996, J. Clin. Invest. 98:1313-1323; Jia et al., 1992, J. Biol. Chem. 267:14322-14327; Wang et al., 1991, J. Biol. Chem.
15   266:14004-14010; or Gronke et al., 1990, J. Biol. Chem. 265:8558-8565. Hydroxylase activity is also measured using carbon dioxide ($^{14}CO_2$ capture assay) in a 96-well microtiter plate format (Zhang et al., 1999, Anal. Biochem. 271:137-142. These assays are readily automated and suitable for high throughput screening of candidate compounds to identify those with hydroxylase inhibitory activity.

20   Candidate compound which inhibit HAAH activation of NOTCH are identified by detecting a reduction in activated NOTCH in a cell which expresses or overexpresses HAAH, e.g., FOCUS HCC cells. The cells are cultured in the presence of a candidate compound. Parallel cultures are incubated in the absence of the candidate compound. To evaluate whether the compound inhibits HAAH activation of NOTCH,
25   translocation of activated NOTCH to the nucleus of the cell is measured. Translocation is measured by detecting a 110 kDa activation fragment of NOTCH in the nucleus of the cell. The activation fragment is cleaved from the large (approximately 300 kDa)

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transmembrane NOTCH protein upon activation. Methods of measuring NOTCH translocation are known, e.g, those described by Song et al., 1999, Proc. Natl. Acad. Sci U.S.A. 96:6959-6963 or Capobianco et al., 1997, Mol. Cell Biol. 17:6265-6273. A decrease in translocation in the presence of the candidate compound compared to that in

5   the absence of the compound indicates that the compound inhibits HAAH activation of NOTCH, thereby inhibiting NOTCH-mediated signal transduction and proliferation of HAAH-overexpressing tumor cells.

Methods of screening for compounds which inhibit phosphorylation of IRS are carried out by incubating IRS-expressing cells in the presence and absence of a

10   candidate compound and evaluating the level of IRS phosphorylation in the cells. A decrease in phosphorylation in cells cultured in the presence of the compound compared to in the absence of the compound indicates that the compound inhibits IRS-1 phosphorylation, and as a result, growth of HAAH-overexpressing tumors. Alternatively, such compounds are identified in an *in vitro* phosphorylation assay known in the art, e.g.,

15   one which measured phosphorylation of a synthetic substrate such as poly (Glu/Tyr).

Example 1: Increased expression of HAAH is associated with malignant transformation

HAAH is a highly conserved enzyme that hydroxylates EGF-like domains in transformation associated proteins. The HAAH gene is overexpressed in many cancer types including human hepatocellular carcinomas and cholangiocarcinomas. HAAH

20   gene expression was found to be undetectable during bile duct proliferation in both human disease and rat models compared to cholangiocarcinoma. Overexpression of HAAH in NIH-3T3 cells was associated with generation of a malignant phenotype, and enzymatic activity was found to be required for cellular transformation. The data described below indicate that overexpression of HAAH is linked to cellular

25   transformation of biliary epithelial cells.

To identify molecules that are specifically overexpressed in transformed malignant cells of human hepatocyte origin, the FOCUS hepatocellular carcinoma (HCC)

cell line was used as an immunogen to generate monoclonal antibodies (mAb) that specifically or preferentially recognize proteins associated with the malignant phenotype. A lambda GT11 cDNA expression library derived from HepG2 HCC cells was screened, and a HAAH-specific mAb produced against the FOCUS cell line was found to recognize

5   an epitope on a protein encoded by an HAAH cDNA. The HAAH enzyme was found to be upregulated in several different human transformed cell lines and tumor tissues compared to adjacent human tissue counterparts. The overexpressed HAAH enzyme in different human malignant tissues was found to be catalytically active.

HAAH gene expression was examined in proliferating bile ducts and in NIH

10   3T3 cells. Its role in the generation of the malignant phenotype was measured by the formation of transformed foci, growth in soft agar as an index of anchorage independent growth and tumor formation in nude mice. The role of enzymatic activity in the induction of transformed phenotype was measured by using a cDNA construct with a mutation in the catalytic site that abolished hydroxylase activity. The results indicated

15   that an increase in expression of HAAH gene is associated with malignant transformation of bile ducts.

The following materials and methods were used to generate the data described below.

Antibodies

20   The FB50 monoclonal antibody was generated by cellular immunization of Balb/C mice with FOCUS HCC cells. A monoclonal anti-Dengue virus antibody was used as a non-relevant control. The HBOH2 monoclonal antibody was generated against a 52 kDa recombinant HAAH polypeptide and recognizes the catalytic domain of beta-hydroxylase from mouse and human proteins. Polyclonal anti-HAAH antibodies cross-

25   react with rat hydroxylase protein. Control antibody anti-Erk-1 was purchased from Santa Cruz Biotechnology, Inc., CA. Sheep anti-mouse and donkey anti-rabbit antisera

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labeled with horseradish peroxidase were obtained from Amersham, Arlington Heights, IL.

Constructs

The murine full length AAH construct (pNH376) and the site-directed

5   mutation construct (pNH376-H660) with abolished catalytic activity were cloned into the eukaryotic expression vector pcDNA3 (Invitrogen Corp., San Diego, CA). The full length human AAH was cloned into prokaryotic expression vector pBC-SK+ (Stratagene, La Jolla, CA). The full length human AAH (GENBANK Accession No. S83325) was subcloned into the EcoRI site of the pcDNA3 vector.

10   Animal model of bile duct proliferation

Rats were divided into 9 separate groups of 3 animals each except for group 9, which contained 5 rats. Group 1 was the non-surgical control group, and group 2 was the sham-operated surgical control. The remaining groups underwent common bile duct ligation to induce intrahepatic bile duct proliferation and were evaluated at 6, 12, 24, 48

15   hours and 4, 8 and 16 days as shown in Table 3. Animals were asphyxiated with CO_2, and liver samples were taken from left lateral and median lobes, fixed in 2 % paraformaldehyde and embedded in paraffin. Liver samples (5 μm) were cut and stained with hematoxylin and eosin to evaluate intrahepatic bile duct proliferation. Immunohistochemistry was performed with polyclonal anti-HAAH antibodies that

20   cross-react with the rat protein to determine levels of protein expression.

Bile duct proliferation associated with primary sclerosing cholangitis (PSC)

Liver biopsy samples were obtained from 7 individuals with PSC and associated bile duct proliferation. These individuals were evaluated according to standard gastroenterohepatological protocols. Patients were 22-46 years of age and

25   consisted of 4 males and 3 females. Four had associated inflammatory bowel disease (3 ulcerative colitis and 1 Crohn's colitis). All patients underwent a radiological evaluation including abdominal ultrasonography and endoscopic retrograde

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cholangiopancreaticography to exclude the diagnosis of extrahepatic biliary obstruction. Tissue sections were prepared from paraffin embedded blocks and were evaluated by hematoxylin and eosin staining for bile duct proliferation. Expression of HAAH was determined by immunohistochemistry using an HAAH-specific monoclonal antibody

5 such as FB50.

Immunohistochemistry

Liver tissue sections (5 μm) were deparaffinized in xylene and rehydrated in graded alcohol. Endogenous peroxidase activity was quenched by a 30-minute treatment with 0.6 % H_2O_2 in 60% methanol. Endogenous biotin was masked by incubation with

10 avidin-biotin blocking solutions (Vector Laboratories, Burlingame, CA). The FB50 mAb (for PSC samples) and polyclonal anti-HAAH-hydroxylase antibodies (for rat liver samples) were added to slides in a humidified chamber at 4°C overnight. Immunohistochemical staining was performed using a standard avidin-biotin horseradish peroxidase complex (ABC) method using Vectastain Kits with diaminobenzidine (DAB)

15 as the chromogen according to manufacturer's instructions (Vector Laboratories, Inc., Burlingame, CA). Tissue sections were counterstained with hematoxylin, followed by dehydration in ethanol. Sections were examined by a light microscopy for bile duct proliferation and HAAH protein expression. Paraffin sections of cholangiocarcinoma and placenta were used as positive controls, and hepatosteatosis samples were used as a

20 negative controls. To control for antibody binding specificity, adjacent sections were immunostained in the absence of a primary antibody, or using non-relevant antibody to Dengue virus. As a positive control for tissue immunoreactivity, adjacent sections of all specimens were immunostained with monoclonal antibody to glyceraldehyde 3-phosphate dehydrogenase.

25 Western blot analysis

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Cell lysates were prepared in a standard radioimmunoprecipitation assay

(RIPA) buffer containing protease inhibitors. The total amount of protein in the lysates

was determined by Bio-Rad colorimetric assay (Bio Rad, Hercules, CA) followed by

10% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE),

5   transferred to PVDF membranes, and subjected to Western blot analysis using FB50,

HBOH2, anti-Erk-1 (used as an internal control for protein loading) as primary, sheep

anti-mouse and donkey anti-rabbit antisera labeled with horseradish peroxidase as

secondary antibodies. Antibody binding was detected with enhanced chemiluminescence

reagents (SuperSignal, Pierce Chemical Company, Rockford, IL) and film

10   autoradiography. The levels of immunoreactivity were measured by volume

densitometry using NIH Image software.

Enzymatic activity assay

AAH activity was measured in cell lysates using the first EGF-like domain of

bovine protein S as substrate where ^{14}C-labeled alpha-ketogluterate hydroxylates the

15   domain releasing ^{14}C containing CO_2 according to standard methods, e.g., those

described by Jia et al., 1992, J. Biol. Chem. 267:14322-14327; Wang et al., 1991, J. Biol.

Chem. 266:14004-14010; or Gronke et al., 1990, J. Biol. Chem. 265:8558-8565.

Incubations were carried out at 37°C for 30 min in a final volume of 40 µl containing 48

µg of crude cell extract protein and 75 µM EGF substrate.

20   Cell transfection studies

The NIH-3T3 cells were cultured in Dulbecco's modified Eagle's medium

(DMEM; Mediatech, Washington, DC) supplemented with 10 % heat-inactivated fetal

calf serum (FCS; Sigma Chemical Co., St.Louis, MO), 1% L-glutamine,

1% non-essential amino acids and 1% penicillin-streptomycin (GIBCO BRL, Life

25   Technologies, Inc., Grand Island, NY). Subconfluent NIH-3T3 cells (3 x 10^5

cells/60-mm dish) were transfected with 10 µg of one of the following plasmids:

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1) non-recombinant pcDNA3 vector (Invitrogen Corp., San Diego, CA) as a negative control; 2) pNH376-H660, the murine AAH cDNA that was mutated in the catalytic domain and cloned into the pcDNA3 vector driven by a CMV promoter; 3) pNH376, the wild type murine AAH cDNA cloned into the pcDNA3 vector; 4) pCDHH, wild type human AAH cDNA cloned into the pcDNA3 vector; or 5) pLNCX-UP1, a cDNA that encodes v-Src oncogene (positive control). Cells were transfected using the calcium phosphate transfection kit according to manufacturer's instructions (5 Prime - 3 Prime, Inc., Boulder, CO). Comparison of cellular transfection efficiency was assessed with the various constructs. For this procedure, confluent plates obtained 48 hours after transfection were split and reseeded into 12 separate 6-cm dishes, and 6 of them were made to grow in the presence of 400 µg/ml G-418 (GIBCO BRL, Life Technologies, Inc., Grant Island, NY) containing medium. The number of G-418 resistant foci was determined at 14 days after transfection and used to correct for any variability in transfection efficiency.

Transformation assay

The NIH-3T3 cells were transfected with the various constructs and allowed to reach confluence after 48 hours as described above. Each 6 cm dish was split and seeded into 12 different 6 cm dishes. While 6 of them were made to grow in the presence of G-418 to detect transfection efficiency, the other six were grown in complete medium without G-418 and with a medium change every 4th day. The number of transformed foci were counted in these plates without G-418 and expressed as transformed foci per µg transfected DNA.

Anchorage-independent cell growth assay

A limiting dilution technique (0.15 cell/well of a flat bottom 96-well-plate) was performed on transfectants grown in G-418 in order to isolate cell clones with different levels of HAAH activity as measured by Western blot analysis and enzymatic

assay of hydroxylase activity. Cloned cell lines (1.0×10^4 cells) were suspended in complete medium containing 0.4 % low-melting agarose (SeaPlaque GTG Agarose; FMC Bioproducts, Rockland, Maine) and laid over a bottom agar mixture consisting of complete medium with 0.53 % low-melting agarose. Each clone was assayed in

5   triplicate. The clones were seeded under these conditions and 10 days later the size (positive growth > 0.1 mm in diameter) and number of foci were determined.

Tumorigenicity in nude mice

The same clones as assessed in the anchorage independent growth assay were injected into nude mice and observed for tumor formation. Tumorigenicity was

10   evaluated using 10 animals in each of 4 groups (Charles River Labs., Wilmington, MA). Group 1 received 1×10^7 cells stably transfected with mock DNA, Group 2-4 received 1 $\times 10^7$ cells of clones stable transfected with pNH376 and expressing various levels of murine HAAH protein. Nude mice were kept under pathogen-free conditions in a standard animal facility. Thirty days after tumor cell inoculation, the animals were

15   sacrificed using isofluorane (Aerrane, Anaquest, NJ) containing chambers and the tumors were carefully removed and weight determined.

Animal model of bile duct proliferation

Following ligation of the common bile duct, intrahepatic bile duct proliferation was evident at 48 hours. Tissue samples obtained 8 and 16 days following

20   common bile duct ligation revealed extensive bile duct proliferation as shown in Table 3.

Table 3: Bile duct proliferation and HAAH expression
at different intervals after common bile duct ligation

Group	Surgical Procedure	Microscopy*	Immunohisto-chemistry
1	no surgery	normal	negative
2	sham surgery	normal	negative
3	6 hours post	normal	negative

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	ligation		
4	12 hours post ligation	normal	negative
5	24 hours post ligation	normal	negative
6	48 hours post ligation	minimal bile duct prolif.	negative
7	4 days post ligation	moderate bile duct prolif.	negative
8	8 days post ligation	extensive bile duct prolif.	negative
9	16 days post ligation	extensive bile duct prolif.	negative

* Investigation was performed under light microscopy following a hematoxylin and eosin staining.

Immunohistochemical staining failed to detect presence of HAAH in proliferating bile ducts at any time. Analysis of HAAH expression in bile ducts derived from sham surgical controls was also negative, while all samples exhibited positive immunoreactivity with control antibodies to glyceraldehyde 3-phosphate dehydrogenase.

5   Thus, bile duct proliferation was not associated with increased HAAH expression in this standard animal model system.

HAAH expression in PSC

The liver biopsy specimens from patients with PSC exhibited bile duct proliferation accompanied by periductal fibrosis and a mononuclear inflammatory cell

10   infiltrate without evidence of dysplasia. Adjacent sections immunostained with the an HAAH-specific monoclonal antibody had no detectable HAAH immunoreactivity in proliferating bile ducts. In contrast, sections of cholangiocarcinoma that were immunostained simultaneously using the same antibody and detection reagents manifested intense levels of HAAH immunoreactivity in nearly all tumor cells, whereas

15   adjacent sections of the cholangiocarcinomas exhibited a negative immunostaining reaction with monoclonal antibody to Dengue virus. These findings indicate that HAAH expression was associated with malignant transformation rather than non-cancerous cellular proliferation of intrahepatic bile ducts.

HAAH associated transformation of NIH-3T3 cells

The transforming capability of the murine and human AAH genes, as well as the murine AAH mutant construct without enzymatic activity were compared to mock DNA (negative control) and v-Src transfected NIH-3T3 cells (positive control). The transforming capability of murine AAH was found to be 2-3 times that of vector DNA

5   control as shown in Fig. 1. The transforming capacity of the human gene was greater than that observed with the murine AAH (32 ± 1.5 versus 13 ± 2.6 transformed foci, respectively). The murine and human AAH transfected cells formed large foci, resembling those of v-Src transfected fibroblasts, compared to the occasional much smaller foci observed in cells transfected with vector DNA that displayed the contact

10   inhibition of fibroblast cell lines. Parallel experiments performed using the mutant pNH376-H660 construct without enzymatic activity revealed no transforming activity. This finding indicates that the enzymatic activity of HAAH is required for the transforming activity exhibited by the HAAH gene.

Anchorage-independent cell growth assay

15   After transient transfection with the murine AAH construct, several different transformed foci were isolated for dilutional cloning experiments to establish stable transfected cell clones with different levels of HAAH gene expression. Nine different cloned cell lines were selected for further study. The expression level of the HAAH protein was determined by Western blot analysis. Clones 7 and 18 had a modest increase

20   in HAAH protein expression, yet formed large colonies in soft agar (Fig. 2). Protein loading was equivalent in all lanes as shown by immunoblotting of the same membranes with an anti-Erk-1 monoclonal antibody. The increased protein expression was associated with increased enzymatic activity as shown in Fig. 3. The capability of these clones to exhibit anchorage independent cell growth in soft agar is presented in Fig. 3.

25   All 3 clones with increased HAAH gene expression demonstrated anchorage independent cell growth compared to the mock DNA transfected clone.

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<u>Tumor formation in nude mice</u>

The 3 clones with increased HAAH gene expression were evaluated for the
ability to form tumors in nude mice. Tumor size in the mouse given clone 18 was
compared to a mock DNA transfected clone. Clones 7, 16 and 18 were highly

5   transformed in this assay and produced large tumors with a mean weight of 2.5, 0.9 and
1.5 grams, respectively (Fig. 4). These data indicate that overexpression of HAAH
contributes to induction and maintenance of the malignant phenotype *in vivo*.

<u>High level HAAH expression is indicative of malignancy</u>

In order to determine if HAAH expression was associated with malignancy

10   rather than increased cell turnover, two models of bile duct proliferation were studied. In
the animal model, ligation of the common bile duct induced extensive intrahepatic bile
duct proliferation, yet there was no evidence of HAAH gene expression under these
experimental conditions as shown in Table 3. Similarly, HAAH gene expression was
assessed in a human disease model associated with bile duct proliferation since PSC is an

15   autoimmune liver disease associated with destruction as well as proliferation of the intra
and extrahepatic bile ducts. PSC is premalignant disease, and a significant proportion of
affected individuals will eventually develop cholangiocarcinoma. However, no evidence
for increased HAAH gene expression in the presence of extensive bile duct proliferation.

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Having established that HAAH protein levels were elevated in cholangiocarcinoma and not in normal or proliferating bile ducts, the role of HAAH in the generation of a malignant phenotype was studied. The HAAH gene was transfected into NIH-3T3 cells and cellular changes, e.g., increased formation of transformed foci,

5   colony growth in soft agar and tumor formation in nude mice associated with malignant transformation, were evaluated. The full-length murine and human AAH genes were cloned into expression constructs and transiently transfected into NIH-3T3 cells. An increased number of transformed foci was detected in cells transfected both with the murine and human AAH genes as compared to mock DNA transfected controls. The

10   increased number of transformed foci, after controlling for transfection efficiency, was not as high compared to v-Src gene transfected cells used as a positive control. The enzymatic activity of the HAAH gene was required for a malignant phenotype because a mutant construct which abolished the catalytic site had no transforming properties. Several stable transfectants and cloned NIH-3T3 cell lines with a modest increase in

15   HAAH protein levels and enzymatic activity were established. Such cell lines were placed in soft agar to examine anchorage independent cell growth as another property of the malignant phenotype. All cell lines grew in soft agar compared to mock DNA transfected control, and there was a positive correlation between the cellular level of HAAH gene expression and the number and size of colonies formed. Three of these

20   cloned cell lines formed tumors in nude mice. All three cell lines with increased HAAH expression were oncogenic as shown by the development of large tumors as another well-known characteristic of the transformed phenotype.

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To determine whether cellular changes induced by overexpression of HAAH were related to the enzymatic function, a site-directed mutation was introduced into the gene that changed the ferrous iron binding site from histidine to lysine at 660th position of mouse HAAH thereby abolishing hydroxylase activity of the murine HAAH. A

5 corresponding mutation in HAAH is used as a dominant negative mutant to inhibit HAAH hydroxylase activity. The pNH376-H660 construct had no transformation activity indicating cellular changes of the malignant phenotype induced by overexpression depends on the enzymatic activity of the protein.

Notch receptors and their ligands have several EGF-like domains in the

10 N-terminal region that contain the putative consensus sequence for beta-hydroxylation. Notch ligands are important elements of the Notch signal transduction pathway and interaction of Notch with its ligands occurs by means of EGF-like domains of both molecules. Point mutations affecting aspartic acid or asparagine residues in EGF-like domains that are the targets for beta-hydroxylation by HAAH reduce calcium binding and

15 protein-protein interactions involved in the activation of downstream signal transduction pathways. Overexpression of HAAH and Notch protein hydroxylation by HAAH contributes to malignancy. Tumor growth is inhibited by decreasing Notch protein hydroxylation by HAAH.

The data presented herein is evidence that high-level HAAH expression is linked to malignant transformation. An increase in expression of the HAAH cDNA in NIH-3T3 cells induced a transformed phenotype manifested by increased numbers of transformed foci, anchorage-independent growth, and tumorigenesis in nude mice. In addition, intact HAAH-enzyme was found to be required for HAAH-associated transformation. Accordingly, inhibition of as little as 20% of endogenous HAAH enzymatic activity or expression confers a therapeutic benefit. For example, clinical benefit is achieved by 50%-70% inhibtion of HAAH expression or activity after administaration of an HAAH inhibitory compound compared to the level associated with untreated cancer cell or a normal noncancerous cell.

HAAH is regulated at the level of transcription. Only modest increases in HAAH expression and enzyme activity were required for cellular transformation. These results indicate that increased HAAH gene expression and enzyme activity contribute to the generation or maintenance of the transformed phenotype and that decreasing transcription of the HAAH gene or decreasing enzymatic activity of the HAAH gene product leads to a decrease in malignancy. Accordingly, HAAH transcription is inhibited by administering compounds which decrease binding of Fos and/or Jun (elements which regulate HAAH transcription) to HAAH promoter sequences.

Since HAAH is up-regulated with malignant transformation of bile duct epithelium, and HAAH immunoreactivity is detectable on tumor cell surface membranes, HAAH is also a molecule to which to target a cytotoxic agent, e.g., by linking the cytotoxic agent to a compound that binds to HAAH expressed on the surface of a tumor cell. Assay of HAAH protein levels in either biological fluids such as bile, or cells obtained by fine needle aspiration is a diagnostic marker of human cholangiocarcinoma.

Example 2: Expression of AAH and growth and invasiveness of malignant CNS neoplasms

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AAH is abundantly expressed in carcinomas and trophoblastic cells, but not in most normal cells, including those of CNS origin. High levels of AAH expression were observed in 15 of 16 glioblastomas, 8 of 9 anaplastic oligodendrogliomas, and 12 of 12 primitive neuroectodermal tumors (PNETs). High levels of AAH immunoreactivity were

5   primarily localized at the infiltrating edges rather than in the central portions of tumors. Double-label immunohistochemical staining demonstrated a reciprocal relationship between AAH and tenascin, a substrate for AAH enzyme activity. PNET2 neuronal cell lines treated with phorbol ester myristate or retinoic acid to stimulate neuritic extension and invasive growth exhibited high levels of AAH expression, whereas H_2O_2-induced

10   neurite retraction resulted in down-regulation of AAH. PNET2 neuronal cells that stably over-expressed the human AAH cDNA had increased levels of PCNA and Bcl-2, and reduced levels of p21/Wafl and p16, suggesting that AAH overexpression results in enhanced pathological cell proliferation, cell cycle progression, and resistance to apoptosis. In addition, the reduced levels of p16 observed in AAH-transfectants indicate

15   that AAH over-expression confers enhanced invasive growth of neoplastic cells since deletion or down-regulation of the p16 gene correlates with more aggressive and invasive in vivo growth of glioblastomas. Increased AAH immunoreactivity was detected at the infiltrating margins of primary malignant CNS neoplasms, further indicating a role of HAAH in tumor invasiveness.

20   The following materials and methods were used to generate the data described below.

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Analysis of AAH Immunoreactivity in Primary Human Malignant CNS
Neoplasms:

AAH immunoreactivity was examined in surgical resection specimens of
glioblastoma (N=16), anaplastic oligodendroglioma (N=9), and primitive

5 neuroectodermal tumor (PNET; supratentorial neuroblastomas (N=3) and
medulloblastomas (N=9). The histopathological sections were reviewed to confirm the
diagnoses using standard criteria. Paraffin sections from blocks that contained
representative samples of viable solid tumor, or tumor with adjacent intact tissue were
studied. Sections from normal adult postmortem brains (N=4) were included as negative

10 controls. AAH immunoreactivity was detected using qn HAAH-specific monoclonal
antibody. Immunoreactivity was revealed by the avidin-biotin horseradish peroxidase
complex method (Vector ABC Elite Kit; Vector Laboratories, Burlingame, CA) using
3-3' diaminobenzidine (DAB) as the chromogen (24) and hematoxylin as a counterstain.

Tenascin and laminin are likely substrates for AAH due to the presence of

15 EGF-like repeats within the molecules. Double-immunostaining studies were performed
to co-localize AAH with tenascin or laminin. The AAH immunoreactivity was detected
by the ABC method with DAB as the chromogen, and tenascin or laminin
immunoreactivity was detected by the avidin-biotin alkaline phosphatase complex
method (Vector Laboratories, Burlingame, CA) with BCIP/NBT as the substrate. As

20 positive and negative controls, adjacent sections were immunostained with monoclonal
antibody to glial fibrillary acidic protein (GFAP) and Hepatitis B surface antigen. All
specimens were batch immunostained using the same antibody dilutions and
immunodetection reagents.

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Cell Lines and Culture Conditions

Studies were conducted to determine whether AAH expression was modulated with neurite (filopodia) extension (sprouting) as occurs with invasive growth of malignant neoplasms. Human PNET2 CNS-derived and SH-Sy5y neuroblastoma cells

5   were cultured and stimulated for 0, 1, 2, 3, 5, or 7 days with 100 nM phorbol 12-ester 13-acetate or 10 µM retinoic acid to induce sprouting. In addition, to examine the effects of neurite retraction on AAH expression, subconfluent cultures were treated for 24 hours with low concentrations (10-40 µM) of H_2O_2. For both studies, AAH expression was evaluated by Western blot analysis using the an HAAH-specific antibody.

10   ### Generation of PNET2 AAH-transfected Clones

The full-length human AAH cDNA (SEQ ID NO:3) was ligated into the pcDNA3.1 mammalian expression vector in which gene expression was under the control of a CMV promoter (Invitrogen Corp., San Diego, CA). PNET2 cells were transfected with either pHAAH or pcDNA3 (negative control) using Cellfectin reagent (Gibco BRL,

15   Grand Island, NY). Neomycin-resistant clones were selected for study if the constitutive levels of AAH protein expression were increased by at least two-fold relative to control (pcDNA3) as detected by Western blot analysis. To determine how AAH overexpression altered the expression of genes that modulate the transformed phenotype, the levels of proliferating cell nuclear antigen (PCNA), p53, p21/Waf1, Bcl-2, and p16 were measured

20   in cell lysates prepared from subconfluent cultures of AAH (N=5) and pcDNA3 (N=5) stably transfected clones. PCNA was used as marker of cell proliferation. p53, p21/Waf1, and Bcl-2 levels were examined to determine whether cells that over-expressed AAH were more prone to cell cycle progression and more resistant to apoptosis. The levels of p16 were assessed to determine whether AAH over-expression

25   has a role in tumor invasiveness.

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<u>Western blot analysis</u>

Cells grown in 10 cm^2 dishes were lysed and homogenized in a standard radioimmunoprecipitation assay RIPA buffer containing protease and phosphatase

5   inhibitors. The supernatants collected after centrifuging the samples at 12,000 x g for 10 minutes to remove insoluble debris were used for Western blot analysis. Protein concentration was measured using the BCA assay (Pierce Chemical Co, Rockford, IL). Samples containing 60 µg of protein were electrophoresed in sodium dodecyl sulfate polyacrylamide gels (SDS-PAGE) and subjected to Western blot analysis. Replicate

10   blots were probed with the individual antibodies. Immunoreactivity was detected with horseradish peroxidase conjugated IgG (Pierce Chemical Co, Rockford, IL) and enhanced chemiluminescence reagents. To quantify the levels of protein expression, non-saturated autoradiographs were subjected to volume densitometry using NIH Image software, version 1.6. Statistical comparisons between pHAAH and pcDNA3 transfected cells

15   were made using Student T tests.

<u>Antibodies</u>

HAAH-specific monoclonal antibody generated against the FOCUS hepatocellular carcinoma cells were used to detect AAH immunoreactivity. Monoclonal antibodies to tenascin, and glial fibrillary acidic protein, and rabbit polyclonal antibody to

20   laminin were purchased from Sigma Co. (St. Louis, MO). Rabbit polyclonal antibody to human p16 was purchased from Santa Cruz Biotechnology Inc. (Santa Cruz, CA). The 5C3 negative control monoclonal antibody to Hepatitis B surface antigen was generated using recombinant protein and used as a negative control.

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AAH immunoreactivity in primary malignant brains tumors

AAH immunoreactivity was detected in 15 of 16 glioblastomas, 8 of 9
anaplastic oligodendrogliomas, and all 12 PNETs. AAH immunoreactivity was localized
5   in the cytoplasm, nucleus, and cell processes. The tissue distribution of AAH
immunoreactivity was notable for the intense labeling localized at the interfaces between
tumor and intact brain, and the conspicuously lower levels of immunoreactivity within
the central portions of the tumors. High levels of AAH immunoreactivity were also
observed in neoplastic cells distributed in the subpial zones, leptomeninges,
10   Virchow-Robin perivascular spaces, and in individual or small clusters of neoplastic cells
that infiltrated the parenchyma. In contrast, AAH immunoreactivity was not detectable in
normal brain. The distribution of AAH immunoreactivity appeared not to be strictly
correlated with DNA synthesis since the density of nuclei in mitosis (1-5%) was similar
in the central and peripheral portions of the tumors.

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Relationship between AAH and tenascin immunoreactivity in glioblastomas

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Tenascin is an extracellular matrix-associated antigen expressed in malignant gliomas. Tenascin contains EGF-like domains within the molecule, a substrate for HAAH hydroxylation. To localize AAH in relation to tenascin immunoreactivity in malignant brain tumors, double-label immunohistochemical staining was performed in

5   which AAH was detected using a brown chromogen (DAB), and tenascin, a blue chromogen (BCIP/NBT). Adjacent sections were similarly double-labeled to co-localize AAH with laminin, another EGF domain containing extracellular matrix molecule expressed in the CNS. Intense levels of tenascin immunoreactivity were observed in perivascular connective tissue and in association with glomeruloid proliferation of

10 endothelial cells. The double-labeling studies demonstrated a reciprocal relationship between AAH and tenascin immunoreactivity such that high levels of AAH were associated with low or undetectable tenascin, and low levels of AAH were associated with abundant tenascin immunoreactivity. Although laminins are also likely substrates for AAH enzyme activity due to the EGF repeats within the molecules, double labeling

15 studies revealed only low levels of laminin immunoreactivity throughout the tumors and at interfaces between tumor and intact tissue.

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<u>Analysis of AAH expression in neuronal cell lines treated with PMA or RA</u>

Neuritic sprouting/filopodia extension marks invasive growth of neoplastic

neuronal cells. PMA activates protein kinase C signal transduction pathways that are

involved in neuritic sprouting. Retinoic acid binds to its own receptor and the

5   ligand-receptor complex translocates to the nucleus where it binds to specific consensus

sequences present in the promoter/enhancer regions of target genes involved in neuritic

growth. Both PNET2 and SH-Sy5y cells can be induced to sprout by treatment with

PMA (60-120 nM) or retinoic acid (5-10 µM). Figs. 5A-D depict data from

representative Western blot autoradiographs; the bar graphs correspond to the mean $\pm$

10   S.D. of results obtained from three experiments. Western blot analysis with the FB50

antibody detected doublet bands corresponding to protein with an molecular mass of

approximately 85 kDa. Untreated PNET2 cells had relatively low levels of AAH

immunoreactivity (Fig. 5A), whereas untreated SH-Sy5y cells had readily detected AAH

expression (Fig. 5B). Untreated PNET2 cells exhibited polygonal morphology with

15   coarse, short radial cell processes, whereas SH-Sy5y cells were slightly elongated and

spontaneously extend fine tapered processes. Both cell lines manifested time-dependent

increases in the levels of AAH immunoreactivity following either RA (Figs. 5A and 5B)

or PMA (Fig. 5C) stimulation and neurite extension. In PNET2 cells, the levels of AAH

protein increased by at least two-fold 24 hours after exposure to RA or PMA, and high

20   levels of AAH were sustained throughout the 7 days of study. In SH-Sy5y cells, the RA-

or PMA-stimulated increases in AAH expression occurred more gradually and were

highest after 7 days of treatment (Fig. 5B).

To examine the effect of AAH expression on neurite retraction, PNET2 and SH-Sy5y cells were treated with low concentrations (8-40 μM) of H_2O_2. After 24 hours exposure to up to 40 μM H_2O_2, although most cells remained viable (Trypan blue dye exclusion), they exhibited neurite retraction and rounding. Western blot analysis using the FB50 antibody demonstrated H_2O_2 dose-dependent reductions in the levels of AAH protein (Fig. 5D).

Effects of AAH over-expression in PNET2 cells

To directly assess the role of AAH overexpression in relation to the malignant phenotype, PNET2 cells were stably transfected with the human full-length cDNA with gene expression under control of a CMV promoter (pHAAH). Neomycin-resistant clones that had at least two-fold higher levels of AAH immunoreactivity relative to neomycin-resistant pcDNA3 (mock) clones were studied. Since aggressive behavior of malignant neoplasms is associated with increased DNA synthesis, cell cycle progression, resistance to apoptosis, and invasive growth, the changes in phenotype associated with constitutive over-expression of AAH were characterized in relation to PCNA, p21/Wafl, p53, Bcl-2, and p16. PCNA was used as an index of DNA synthesis and cell proliferation. p21/Wafl is a cell cycle inhibitor. Expression of the p53 tumor-suppressor gene increases prior to apoptosis, whereas bcl-2 inhibits apoptosis and enhances survival of neuronal cells. p16 is an oncosuppressor gene that is often either down-regulated or mutated in infiltrating malignant neoplasms.

Five pHAAH and 5 pcDNA3 clones were studied. Increased levels of AAH expression in the pHAAH transfected clones was confirmed by Western (Fig. 6) and Northern blot analyses. Western blot analysis using cell lysates from cultures that were 70 to 80 percent confluent demonstrated that constitutively increased levels of AAH expression (approximately 85 kDa; $P<0.05$) in pHAAH-transfected cells were associated with significantly increased levels of PCNA (approximately 35 kDa; $P<0.01$) and Bcl-2

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(approximately 25 kDa; P<0.05), and reduced levels of p21/Waf1 (approximately 21 kDa; P<0.001) and p16 (approximately 16 kDa; P<0.001) (Fig. 6). However, the pHAAH stable transfectants also exhibited higher levels of wild-type p53 (approximately 53-55 kDa). Although AAH expression (85 kDa protein) in the stable transfectants was

5 increased by only 75 to 100 percent, the levels of p16 and p21/Waf1 were sharply reduced, and PCNA increased by nearly two-fold (Fig. 6).

Increased AAH expression is indicative of growth and invasiveness of malignant CNS neoplasms

The data described herein demonstrates that AAH overexpression is a

10 diagnostic tool by which to identify primary malignant CNS neoplasms of both neuronal and glial cell origin. Immunohistochemical staining studies demonstrated that AAH overexpression was detectable mainly at the interfaces between solid tumor and normal tissue, and in infiltrating neoplastic cells distributed in the subpial zones, leptomeninges, perivascular spaces, and parenchyma. *In vitro* experiments demonstrated that AAH gene

15 expression was modulated with neurite (filopodium) extension and invasiveness and down-regulated with neurite retraction. In addition, PNET2 cells stably transfected with the AAH cDNA exhibited increased PCNA and bcl-2, and reduced Waf1/p21 and p16 expression. Therefore, AAH overexpression contributes to the transformed phenotype of CNS cells by modulating the expression of other genes that promote cellular proliferation

20 and cell cycle progression, inhibit apoptosis, or enhance tumor cell invasiveness.

The data demonstrated readily detectable AAH mRNA transcripts (4.3 kB and 2.6 kB) and proteins (85 kDa and 50-56 kDa) in PNET2 and SH-Sy5y cells, but not in normal brain. Correspondingly, high levels of AAH immunoreactivity were observed in 35 of the 37 in malignant primary CNS-derived neoplasms studied, whereas the 4 normal

25 control brains had no detectable AAH immunoreactivity. The presence of high-level AAH immunoreactivity at the infiltrating margins and generally not in the central portions of the tumors indicates that AAH overexpression is involved in the invasive

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growth of CNS neoplasms. Administration of compounds which decrease AAH expression or enzymatic activity inhibits proliferation of CNS tumors which overexpress AAH, as well as metastases of CNS tumors to other tissue types.

The AAH enzyme hydroxylates EGF domains of a number of proteins.

5 Tenascin, an extracellular matrix molecule that is abundantly expressed in malignant gliomas, contains EGF-like domains. Since tenascin promotes tumor cell invasion, its abundant expression in glioblastomas represents an autocrine mechanism of enhanced tumor cell growth vis-a-vis the frequent overexpression of EGF or EGF-like receptors in malignant glial cell neoplasms. Analysis of the functional domains of tenascins indicated

10 that the mitogenic effects of this family of molecules are largely mediated by the fibronectin domains, and that the EGF-like domains inhibit growth, cell process elongation, and matrix invasion. Therefore, hydroxylation of the EGF-like domains by AAH represents an important regulatory factor in tumor cell invasiveness.

Double-label immunohistochemical staining studies demonstrated a reciprocal

15 relationship between AAH and tenascin immunoreactivity such that high levels AAH immunoreactivity present at the margins of tumors were associated with low levels of tenascin, and low levels of AAH were often associated with high levels of tenascin. These observations indicated that AAH hydroxylation of EGF-like domains of tenascin alters the immunoreactivity of tenascin protein, and in so doing, facilitates the invasive

20 growth of malignant CNS neoplasms into adjacent normal tissue and perivascular spaces.

AAH immunoreactivity was examined in PNET2 and SH-Sy5y neuronal cells induced to undergo neurite extension with PMA or retinoic acid, or neurite retraction by exposure to low doses of H_2O_2. AAH expression was sharply increased by PMA- or retinoic acid-induced neurite (filopodium) extension, and inhibited by H_2O_2-induced

25 neurite retraction and cell rounding. Neurite or filopodium extension and attachment to extracellular matrix are required for tumor cell invasion in the CNS. The EGF-like

domains of tenascin inhibit neuritic and glial cell growth into the matrix during development.

To directly examine the role of AAH overexpression in relation to the transformed phenotype, genes modulated with DNA synthesis, cell cycle progression,

5   apoptosis, and tumor invasiveness were examined in neuronal cell clones that stably over-expressed the human AAH cDNA. The findings of increased PCNA and reduced Waf1/p21 immunoreactivity indicated that AAH overexpression enhances cellular proliferation and cell cycle progression. In addition, the finding of increased Bcl-2 expression indicated that AAH overexpression contributes to the transformed phenotype

10 by increasing cellular resistance to apoptosis. The apparently contradictory finding of higher levels of p53 in the cells that overexpressed AAH is explained by the observation that high levels of wildtype p53 in immature neuronal cells were associated with neuritic growth (invasiveness) rather than apoptosis. Levels of p16 were reduced (compared to normal cells) or virtually undetectable in cells that constitutively overexpressed AAH; a

15 deletion mutation of the p16 gene has been correlated with invasive growth and more rapid progression of malignant neoplasms, including those of CNS origin. These data indicate that p16 expression is modulated by AAH.

Example 3: Increased HAAH production and IRS-mediated signal transduction

IRS-1 mediated signal transduction pathway is activated in 95% of human

20 HCC tumors compared to the adjacent uninvolved liver tissue. HAAH is a downstream effector gene involved in this signal transduction pathway. HAAH gene upregulation is closely associated with overexpression of IRS-1 in HCC tumors as revealed by immunohistochemical staining and Western blot analysis. A high level of HAAH protein is expressed in HCC and cholangiocarcinoma compared to normal hepatocytes and bile

25 ducts. Both of these tumors also exhibit high level expression of IRS-1 by immunohistochemical staining. FOCUS HCC cell clones stably transfected with a C-terminal truncated dominant negative mutant of IRS-1, which blocks insulin and IGF-1

54

stimulated signal transduction, was associated with a striking reduction in HAAH gene expression in liver. In contrast, transgenic mice overexpressing IRS-1 demonstrate an increase in HAAH gene expression by Western blot analysis. Insulin stimulation of FOCUS HCC cells (20 and 40 U) in serum free medium and after 16 hr of serum

5   starvation demonstrated upregulation of HAAH gene expression. These data indicate that HAAH gene expression is a downstream effector of the IRS-1 signal transduction pathway.

Example 4: Effects of HAAH expression levels on the characteristics of the malignant phenotype

10   Overexpression of IRS-1 in NIH 3T3 cells induces transformation. The full-length murine HAAH construct was cloned into the pcDNA3 eukaryotic expression vector. A second murine construct encoded HAAH with abolished catalytic activity due to a site directed mutation. The full-length human HAAH cDNA was cloned into the pcDNA3 expression vector as well as a plasmid that encodes v-src which was used as a

15   positive control for transformation activity. Standard methods were used for transfection of NIH 3T3 cells, control for transfection efficiency, assays of HAAH enzymatic activity, transformation by analysis of foci formation, anchorage-independent cell growth assays and analysis of tumorigenicity in nude mice. The data indicated that HAAH overexpression is associated with generation of a malignant phenotype.

20

indicates malignancy

cDNA	# of foci ± S.D.[b]	NIH 3T3 clone	# of colonies[c]
pcDNA3 (mock)	6.0 ± 3.3	PcDNA (mock)	0.4 ± 0.5
murine HAAH	14.0 ± 2.9	clone 18[d]	6.2 ± 2.9
mutant murine HAAH[a]	1.6 ± 1.0	clone 16[e]	4.7 ± 6.5
human HAAH	32.0 ± 5.4		
v-scr	98.0 ± 7.1		

a. enzymatically inactive HAAH
b. P<0.01 compared to mock and mutant murine HAAH
5 c. P<0.001 compared to mock
d. Clone 18 is a stable cloned NIH 3T3 cell line that overexpression human HAAH by approximately two fold.
e. Clone 16 is a stable cloned NIH 3T3 cell line that overexpresses human HAAH by about 50%.

10   These data indicate that overexpression of HAAH is associated with formation

of transformed foci. Enzymatic activity is required for cellular transformation to occur.

Cloned NIH 3T3 cell lines with increased human HAAH gene expression grew as solid

tumors in nude mice. HAAH is a downstream effector gene of the IRS-1 signal

transduction pathway.

15 Example 5: Inhibition of HAAH gene expression

        The FOCUS HCC cell line from which the human HAAH gene was initially

cloned has a level of HAAH expression that is approximately 3-4 fold higher than that

found in normal liver. To make an HAAH antisense construct, the full length human

HAAH cDNA was inserted in the opposite orientation into a retroviral vector containing

a G418 resistant gene, and antisense RNA was produced in the cells. Shorter HAAH antisense nucleic acids, e.g., those corresponding to exon 1 of the HAAH gene are also used to inhibit HAAH expression.

FOCUS cells were infected with this vector and the level of HAAH was

5   determined by Western blot analysis. A reduction in HAAH gene expression was observed. Growth rate and morphologic appearance of cells infected with a retrovirus containing a nonrelevant Green Fluorescent Protein (GFP) also inserted in the opposite orientation as a control (Fig. 8). Cells (harboring the HAAH antisense construct) exhibited a substantial change in morphology characterized by an increase in the

10 cytoplasm to nuclear ratio as well as assuming cell shape changes that were reminiscent of normal adult hepatocytes in culture. Cells with reduced HAAH levels grew at a substantially slower rate than retroviral infected cells expressing antisense (GFP) (control) as shown in Fig. 8. A reduction in HAAH gene expression was associated with a more differentiated noncancerous "hepatocyte like" phenotype. Expression of HAAH

15 antisense sequences are used to inhibit tumor growth rate. Reduction of HAAH cellular levels results in a phenotype characterized by reduced formation of transformed foci, low level or absent anchorage independent growth in soft agar, morphologic features of differentiated hepatocytes as determined by light and phase contrast microscopy, and no tumor formation (as tested by inoculating the cells into nude mice).

20 Example 6: Inhibition of AAH expression by AAH antisense oligonucleotides

Oligonucleotides that inhibit AAH gene expression were designed and synthesized using standard methods. For example, antisense oligonucleotides (20 mers) were designed to bind to the 5' region of the AAH mRNA and overlap with the AUG initiation codon (Table 5). The antisense oligonucleotides were selected such that they

25 were complementary to sequences beginning 1 (Location -1), 6 (Location -6), or 11 (Location -11) nucleotides upstream (prior to) the "A" of the AUG (methionine) codon. In addition, a sense oligonucleotide beginning at Location -3 was made.

57

Table 5: Sequence of exemplary oligonucleotide molecules

Location (-1)
5' CAT TCT TAC GCT GGG CCA TT 3' (SEQ ID NO:10)

5   Location (-6)
5' TTA CGC TGG GCC ATT GCA CG 3' (SEQ ID NO:11)

Location (-11)
5' CTG GGC CAT TGC ACG GTC CG 3' (SEQ ID NO:12)
10

Sense
5' ATC ATG CAA TGG CCC AGC GTA A 3' (SEQ ID NO:13)

Fig. 10 shows the region of the AAH gene to which the antisense oligonucleotides

described in Table 5 bind. All of the oligonucleotides were designed using MacVector

15   6.5.3 software.

AAH antisense oligonucleotides tested were found to inhibit AAH gene

expression. Using an *in vitro* cell free transcription translation assay (TNT Quick

Coupled System), the human AAH cDNA (pHAAH) was used to synthesize AAH

protein. *In vitro* translation was achieved with rabbit reticulocyte lysate included in the

20   reaction mixture. The translated product was labeled with [^{35}S] methionine in the

presence of reaction buffer, RNA polymerase, amino acid mixture, and ribonuclease

inhibitor (RNAsin). The products were analyzed by SDS-PAGE followed by

autoradiography. A luciferase (Luc) expressing plasmid was used as a positive control.

In the second and third lanes, synthesis of the ~85 kD AAH protein is shown (AAH,

25   arrow) using 1 or 2 micrograms of plasmid as the template and the T7 DNA-dependent

RNA polymerase primer/promoter to generate mRNA. The addition of 100x or 1000x

excess antisense oligonucleotide primer resulted in progressively greater degrees of

inhibition of AAH protein synthesis, whereas the inclusion of the same amounts of sense

oligonucleotide had no effect on AAH protein synthesis. Further studies demonstrated

30   complete inhibition of AAH protein synthesis only with the antisense oligonucleotides.

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In addition, effective inhibition of gene expression was observed using all three antisense oligonucleotides tested. Fig. 11 shows the results of an *in vitro* transcription/translation analysis of AAH antisense oligonucleotides and shows that the antisense oligonucleotides tested block translation of the HAAH RNA and subsequent protein synthesis of HAAH

5   protein.

Inhibition of AAH gene expression was also tested in cells. Fig. 11 shows the results of a Microtiter In situ Luminescence Quantification (MILQ) Assay and demonstrates the actual effect of the antisense oligonucleotides inside cells. Substantial reduction in HAAH gene expression was detected by simply adding the antisense

10   oligonucleotides to the culture medium of the cells. The MILQ assay quantifies *in situ* hybridization binding in cultured cells without the need for RNA extraction. The MILQ assay was used to study competitive antisense binding inhibition to illustrate that the antisense probe hybridized to the mRNA expressed endogenously within the Sh-SySy neuroblastoma cells. In this figure, inhibition of FITC-labeled Location -6 antisense

15   oligonucleotide binding using specific unlabeled antisense oligonucleotides is shown. Minimal inhibition of binding was observed using non-relevant oligonucleotides. The unlabeled specific oligonucleotide was capable of effectively competing for the binding site designated by the FITC-conjugated Location -6 probe, whereas the non-relevant probe exhibited significantly less inhibition at the same molar concentration. Bound

20   probe (FITC-labeled) was detected using horseradish peroxidase conjugated antibodies to FITC, and luminescence reagents were used to detect the bound antibody. Luminescence units were corrected for cell density and are arbitrary in nature. These data indicate that cells effectively take up antisense oligonucleotides in the surrounding environment and that the oligonucleotides taken up effectively and specifically inhibit HAAH gene

25   expression.

Inhibition of HAAH gene expression is enhanced by contacting cells with a phosphorothioate derivative of the HAAH antisense. Phosphorothioate antisense

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derivatives are made using methods well known in the art. ~~Fig. 13 shows inhibition of AAH gene expression due to antisense (Location -6) oligonucleotide gene delivery into SH-SySy neuroblastoma cells.~~ The MILQ assay was used to measure gene expression resulting from antisense oligonucleotide gene delivery. Cells were contacted with AAH Location -6 antisense DNA, and AAH protein expression was measured using methods known in the art, e.g., the MICE assay (de la Monte, et al, 1999, Biotechniques), to determine if it was inhibited by hybridization with the oligonucleotide. The MICE assay is used to measure immunoreactivity in cultured cells without the need to extract proteins or perform gel electrophoresis. This assay is more sensitive than Western blot analysis.

10   Using the MICE assay, AAH immunoreactivity was assessed in cells transfected with non-relevant (random) oligonucleotide sequences, specific antisense oligonucleotides (Location -6), and a phosphorothioate Location -6 antisense oligonucleotide. Phosphorothioate chemical modification of the oligonucleotide was found to permit greater stability of the DNA inside the cell since the sulfur group protects the DNA from

15   the degradation that normally occurs with. phosphodiester bonds and cellular nucleases. Antisense AAH oligonucleotide (Location -6) transfection resulted in reduced levels of AAH immunoreactivity, and using the phosphorothioate linked Location -6 antisense oligonucleotide, the effect of inhibiting AAH gene expression was substantial relative to the levels observed in cells transfected with the random oligonucleotide. The more

20   effective inhibition of AAH expression using the phosphorothioate-linked antisense oligonucleotide was likely due to the greater stability of the molecule combined, with retained effective binding to mRNA.

Example 7: Human IRS-1 mutants

        Insulin/IGF-1 stimulated expression of HAAH in HCC cell lines.

25   Dominant-negative IRS-1 cDNAs mutated in the plextrin and phosphotryosine (PTB) domains, and Grb2, Syp and PI3K binding motifs located in the C-terminus of the molecule were constructed. Human IRS-1 mutant constructs were generated to evaluate

60

how HAAH gene expression is upregulated by activation of the IRS-1 growth factor signal transduction cascade. Specific mutations in the C terminus of the hIRS-1 molecule abolished the various domains which bind to SH2-effector proteins such as Grb2, Syp and PI3K. The human IRS-1 protein contains the same Grb2 and Syp binding motifs of

5 897YVNI (underlined in Table 5, below and 1180YIDL (underlined in Table 5, below), respectively, as the rat IRS-1 protein. Mutants of hIRS-1 were constructed by substitution of a TAT codon (tyrosine) with a TTT codon (phenylalanine), in these motifs by use of oligonucleotide-directed mutagenesis suing the following primers: (5'-GGGGGAATTTGTCAATA-3' (SEQ ID NO:8) and 5'-GAATTTGTTAATATTG-3'

10 (SEQ ID NO:9), respectively). The cDNAs of hIRS-1 (wild-type) and mutants (tyrosine 897-to-phenylalanine and tyrosine 1180-to-phenylalanine) were subcloned into the pBK-CMV expression vector and designated as hIRS-1-wt, 897F, ΔGrb2), 1180F, and ΔSyp.

Table 6: Human IRS-1 amino acid sequence

```
      MASPPESDGF SDVRKVGYLR KPKSMHKRFF VLRAASEAGG PARLEYYENE KKWRHKSSAP 61
      KRSIPLESCF NINKRADSKN KHLVALYTRD EHFAIAADSE AEQDSWYQAL LQLHNRAKGH 121
   5  HDGAAALGAG GGGGSCSGSS GLGEAGEDLS YGDVPPGPAF KEVWQVILKP KGLGQTKNLI 181
      GIYRLCLTSK TISFVKLNSE AAAVVLQLMN IRRCGHSENF FFIEVGRSAV TGPGEFWMQV 241
      DDSVVAQNMH ETILEAMRAM SDEFRPRSKS QSSSNCSNPI SVPLRRHHLN NPPPSQVGLT 301
      RRSRTESITA TSPASMVGGK PGSFRVRASS DGEGTMSRPA SVDGSPVSPS TNRTHAHRHR 361
      GSARLHPPLN HSRSIPMPAS RCSPSATSPV SLSSSSTSGH GSTSDCLFPR RSSASVSGSP 421
  10  SDGGFISSDE YGSSPCDFRS SFRSVTPDSL GHTPPARGEE ELSNYICMGG KGPSTLTAPN 481
      GHYILSRGGN GHRCTPGTGL GTSPALAGDE AASAADLDNR FRKRTHSAGT SPTITHQKTP 541
      SQSSVASIEE YTEMMPAYPP GGGSGGRLPG HRHSAFVPTR SYPEEGLEMH PLERRGGHHR 601
      PDSSTLHTDD GYMPMSPGVA PVPSGRKGSG DYMPMSPKSV SAPQQIINPI RRHPQRVDPN 661
      GYMMMSPSGG CSPDIGGGPS SSSSSSNAVP SGTSYGKLWT NGVGGHHSHV LPHPKPPVES 721
  15  SGGKLLPCTG DYMNMSPVGD SNTSSPSDCY YGPEDPQHKP VLSYYSLPRS FKHTQRPGEP 781
      EEGARHQHLR LSTSSGRLLY AATADDSSSS TSSDSLGGGY CGARLEPSLP HPHHQVLQPH 841
      LPRKVDTAAQ TNSRLARPTR LSLGDPKAST LPRAREQQQQ QQPLLHPPEP KSPGEYVNIE 901
      FGSDQSGYLS GPVAFHSSPS VRCPSQLQPA PREEETGTEE YMKMDLGPGR RAAWQESTGV 961
      EMGRLGPAPP GAASICRPTR AVPSSRGDYM TMQMSCPRQS YVDTSPAAPV SYADMRTGIA 1021
  20  AEEVSLPRAT MAAASSSSAA SASPTGPQGA AELAAHSSLL GGPQGPGGMS AFTRVNLSPN 1081
      RNQSAKVIRA DPQGCRRRHS SETFSSTPSA TRVGNTVPFG AGAAVGGGGG SSSSSEDVKR 1141
      HSSASFENVW LRPGELGGAP KEPAKLCGAA GGLENGLNYI DLDLVKDFKQ CPQECTPEPQ 1201
      PPPPPPPHQP LGSGESSSTR RSSEDLSAYA SISFQKQPED RQ (SEQ ID NO:5; GENBANK
```

Accession No. JS0670; pleckstrin domain spans residues 11-113, inclusive; Phosphate-
binding residues include 46, 465, 551, 612, 632, 662, 732, 941, 989, or 1012 of SEQ ID
NO:5)

Table 7: Human IRS-1 cDNA

```
  30  cggcggcgcg gtcggagggg gccggcgcgc agagccagac gccgccgctt gttttggttg 61
      gggctctcgg caactctccg aggaggagga ggaggaggga ggaggggaga agtaactgca 121
      gcggcagcgc cctcccgagg aacaggcgtc ttccccgaac ccttcccaaa cctcccccat 181
      cccctctcgc ccttgtcccc tcccctcctc cccagccgcc tggagcgagg ggcagggatg 241
      agtctgtccc tccggccggt ccccagctgc agtggctgcc cggtatcgtt tcgcatggaa 301
  35  aagccacttt ctccacccgc cgagatgggc ccggatgggg ctgcagagga cgcgcccgcg 361
      ggcggcggca gcagcagcag cagcagcagc agcaacagca acagccgcag cgccgcggtc 421
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      gcccaaggat atttaatttg cctcgggaat cgctgcttcc agaggggaac tcaggaggga 601
  40  aggcgcgcgc gcgcgcgcgc tcctggaggg gcaccgcagg gacccccgac tgtcgcctcc 661
      ctgtgccgga ctccagccgg ggcgacgaga gatgcatctt cgctccttcc tggtggcggc 721
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63

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aaaaaaaa (SEQ ID NO:6; GENBANK Accession No. NM 005544)
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The double mutation of tyrosine 897 and 1180 was constructed by replacement of 3'-sequences coding 897F by the same region of 1180F using restriction enzymes NheI and EcoRI, and this construct was called 897F1180F or ΔGrb2 ΔSyp. The expression plasmids were under control of a CMV promoter (hIRS-1-wt, ΔGrb2, ΔSyp, ΔGrb2, ΔSyp and pBK-CMV (mock) and linearized at the 3'-end of poly A signal sequences by MluI restriction enzymes followed by purification. A similar approach was used to change the tyrosine residue to phenyalanine at positions 613 and 942 to create the

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double PI3K mutant construct (ΔPI3K). The hIRS-1 mutants have a FLAG epitope (DYKDDDDK (SEQ ID NO:6) + stop codon) added to the C-terminus by PCR. This strategy allows to distinguish the mutant protein from "wild type" hIRS-1 in stable transfected cell lines. The mutants are used to define the link between the IRS signal

5   transduction pathway and activation of HAAH as a downstream effector gene and identify compounds to inhibit transduction along the pathway to inhibit growth of tumors characterized by HAAH overexpression. Antibodies or other compounds which bind to phosphorylation sites or inhibit phosphorylation at those sites are used to inhibit signal transduction and thus proleferation of HAA-overexpressing tumors.

10   Other embodiments are within the following claims.

            What is claimed is: